

SEQUENCE LISTING

<110> Majumder, Kumud  
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Tchernev, Velizar T  
Spytek, Kimberly A  
Li, Li  
Baumgartner, Jason C  
Gusev, Vladimir

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Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His  
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<212> DNA
<213> Homo sapiens
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gtttctgtttt ccacatgtttttt accttggaaac ccagcactgt ttaccttttc aattttggccg 180
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Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu  
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Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala  
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Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Gly  
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Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser  
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Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile  
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165 170 175  
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile  
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Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln  
195 200 205  
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Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg  
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245 250 255  
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
260 265 270  
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe  
275 280 285  
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His  
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Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg  
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 35 40 45

Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His Pro Pro  
 50 55 60

Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val Arg Ile  
 65 70 75 80

Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu Ala Gly  
 85 90 95

Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp Arg Lys  
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Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp Phe Gln  
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Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu Asp Phe  
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Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met Val Thr  
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Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met Ser Val  
 165 170 175

Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg Thr Arg  
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Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp Ser Cys  
 195 200 205

Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu Ala Ala  
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 Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys Val Met  
 225 230 235 240  
 Gly Glu Glu Leu Cys Thr Gly Ala Phe Pro Gly Gln Val Ala Gly Pro  
 245 250 255  
 Arg Gln Ala Val Leu Ala Gly Pro Leu Pro Leu Ala Glu Glu Ala Ala  
 260 265 270  
 Gly Val Pro Ala Tyr Leu Ala Tyr Ile Phe Ile Pro Lys Gln Phe Phe  
 275 280 285  
 Arg Ser Leu Pro Leu Ser Tyr Asp Leu Leu Tyr Phe Pro Pro Leu Ser  
 290 295 300  
 Tyr Pro Ser Val Ile Arg Asn Ile Ser Ser Leu Pro Pro Gln His Asp  
 305 310 315 320  
 Lys Pro Arg Arg Thr Trp Cys Pro Pro Pro Trp Thr Gly Pro Ala Ser  
 325 330 335  
 Pro Asp Gln Ile Glu Asn Thr Tyr Arg Phe Ala Thr Cys Tyr Val His  
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Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile  
35 40 45

Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile  
50 55 60

Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met  
65 70 75 80

Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys  
85 90 95

Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala  
100 105 110

Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro  
115 120 125

Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala  
130 135 140

Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu  
145 150 155 160

Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr  
165 170 175

Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg  
180 185 190

Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp  
195 200 205

Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe  
210 215 220

Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly  
225 230 235 240

Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser  
245 250 255

Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile  
260 265 270

Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val  
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Phe Phe Asn Lys  
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Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu  
35 40 45

Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe  
50 55 60

Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu  
65 70 75 80

Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala  
85 90 95

Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu  
100 105 110

Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
115 120 125

Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly  
130 135 140

Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro  
145 150 155 160

Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu  
165 170 175

Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr  
180 185 190

Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr  
195 200 205

Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu  
210 215 220

Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu  
225 230 235 240

Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro  
245 250 255

Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro  
260 265 270

Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Pro Pro Val  
275 280 285

Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly  
290 295 300

Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe  
305 310 315

<210> 12

<211> 994

<212> DNA

<213> Homo sapiens

<400> 12

tgtctgaatta ctcaaagtca ctatggaga ctggaaataac agtgatgctg tggagccat 60  
atttatccctg aggggttttc ctggactgga gtatgttcat tcttggctct ccatcctctt 120  
ctgtcttgca tattttggtag catttatggg taatgttacc atcctgtctg tcatttggat 180  
agaatcctct ctcacatcagc ccatgttatta ctttatttcc atcttggcag tgaatgacct 240  
ggggatgtcc ctgtctcacac ttcccaccat gcttgcgttg ttatggttgg atgctccaga 300  
gatccaggca agtgcttgct atgctcagct gttcttcatc cacacattca cattcctgga 360  
gtcctcagtg ttgctggcca tggcctttga ccgtttgtt gctatctgcc atccactgca 420  
ctacccacc atcctcacca acagtgtaat tggcaaattt gttttggcct gtttgctacg 480  
aagcttggga gttgtacttc ccacaccttt gctactgaga cactatcaact actgccatgg 540  
caatgccctc tctcacgcct tctgtttgca ccaggatgtt ctaagattat cctgtacaga 600  
tgccaggacc aacagtattt atgggctttt tgtagtcatt gccacactag gtgtggattc 660  
aatcttcata cttctttctt atgttctgat tcttaataact gtgctggata ttgcacatctcg 720  
tgaagagcag ctaaaggcac tcaacacatg tgtatccat atctgtgtgg tgcttatctt 780  
ctttgtgcca gttattgggg tgtcaatggt ccatcgtttt gggaaagcatc tgtctccat 840  
agtccacatc ctcacatggcag acatgtaccc tcttcttccc ccagtcctta accctattgt 900  
ctatagtgtc agaacaattt agatttcgttot aggaatttca cacaagtttgc tcctaaggag 960  
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<210> 13

<211> 315

<212> PRT

<213> Homo sapiens

<400> 13

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu  
1 5 10 15

Arg	Gly	Phe	Pro	Gly	Leu	Glu	Tyr	Val	His	Ser	Trp	Leu	Ser	Ile	Leu
20															30
Phe	Cys	Leu	Ala	Tyr	Leu	Val	Ala	Phe	Met	Gly	Asn	Val	Thr	Ile	Leu
35															45
Ser	Val	Ile	Trp	Ile	Glu	Ser	Ser	Leu	His	Gln	Pro	Met	Tyr	Tyr	Phe
50															60
Ile	Ser	Ile	Leu	Ala	Val	Asn	Asp	Leu	Gly	Met	Ser	Leu	Ser	Thr	Leu
65															80
Pro	Thr	Met	Leu	Ala	Val	Leu	Trp	Leu	Asp	Ala	Pro	Glu	Ile	Gln	Ala
	85								90						95
Ser	Ala	Cys	Tyr	Ala	Gln	Leu	Phe	Phe	Ile	His	Thr	Phe	Thr	Phe	Leu
	100								105						110
Glu	Ser	Ser	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Phe	Val	Ala	Ile
	115								120						125
Cys	His	Pro	Leu	His	Tyr	Pro	Thr	Ile	Leu	Thr	Asn	Ser	Val	Ile	Gly
	130								135						140
Lys	Ile	Gly	Leu	Ala	Cys	Leu	Leu	Arg	Ser	Leu	Gly	Val	Val	Leu	Pro
	145								150						160
Thr	Pro	Leu	Leu	Leu	Arg	His	Tyr	His	Tyr	Cys	His	Gly	Asn	Ala	Leu
	165								170						175
Ser	His	Ala	Phe	Cys	Leu	His	Gln	Asp	Val	Leu	Arg	Leu	Ser	Cys	Thr
	180								185						190
Asp	Ala	Arg	Thr	Asn	Ser	Ile	Tyr	Gly	Leu	Cys	Val	Val	Ile	Ala	Thr
	195								200						205
Leu	Gly	Val	Asp	Ser	Ile	Phe	Ile	Leu	Leu	Ser	Tyr	Val	Leu	Ile	Leu
	210								215						220
Asn	Thr	Val	Leu	Asp	Ile	Ala	Ser	Arg	Glu	Glu	Gln	Leu	Lys	Ala	Leu
	225								230						240
Asn	Thr	Cys	Val	Ser	His	Ile	Cys	Val	Val	Leu	Ile	Phe	Phe	Val	Pro
	245								250						255
Val	Ile	Gly	Val	Ser	Met	Val	His	Arg	Phe	Gly	Lys	His	Leu	Ser	Pro
	260								265						270
Ile	Val	His	Ile	Leu	Met	Ala	Asp	Met	Tyr	Leu	Leu	Leu	Pro	Pro	Val
	275								280						285
Leu	Asn	Pro	Ile	Val	Tyr	Ser	Val	Arg	Thr	Lys	Gln	Ile	Arg	Leu	Gly
	290								295						300
Ile	Leu	His	Lys	Phe	Val	Leu	Arg	Arg	Arg	Phe					
	305								310						315

<210> 14  
 <211> 994  
 <212> DNA  
 <213> Homo sapiens

<400> 14

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ctgtcttgc tatggtag catttatggg taatgttacc atcctgtctg tcattggat 180  
agaatccctct ctccatcagc ccatgttatta ctttatttcc atcttggcag tgaatgacct 240  
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gatccaggca agtgcttgcg atgctcagct gttcttcattc cacacattca cattccttgg 360  
gtcctcagtg ttgctggcca tggccttta ccgtttgtt gctatctgcc atccactgca 420  
ctacccacc atcctcacca acagtgtaat tggcaaaatt gggttggcct gtttgcatacg 480  
aagcttggga gttgtacttc ccacacctt gctactgaga cactatcact actgccatgg 540  
caatgccctc tctcacgcct tctgtttgca ccaggatgtt ctaagattat cctgtacaga 600  
tgccaggacc aacagtattt atgggctttg ttagtgcatt gccacactag gtgtggattc 660  
aatcttcata cttcttctt atgttctgtat tcttaatact gtgctggata ttgcattctcg 720  
tgaagagcag ctaaaggcac tcaacacatg tgtatccat atctgtgtgg tgcttatctt 780  
cttgcgtcca gttatgggg tgcataatggt ccatcgctt gggaaagcattc tgtctccat 840  
agtccacatc ctcatggcag acatctaccc tcttcttccc ccagtccctt accctattgt 900  
ctatagtgtc agaacaaggc agattcgtct aggaattctc cacaagtttg tcctaaggag 960  
gaggttttaa gtaacctctg tcctccaact ttcc 994

<210> 15

<211> 985

<212> DNA

<213> Homo sapiens

<400> 15

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tcacatttt cctcatttgc atcccaggc tggaaagactt ccacatgtgg atctccggc 120  
ctttctgtct tggatccctt gtggctttgc tggcaatgc caccattctg ctatgtcatca 180  
aggtagaaca gactctccgg gagccatgt tctacttccctt ggccattctt tccactattg 240  
atttggccct ttctgcaacc tctgtgcctc gcatgctggg tatcttctgg tttgtatgtc 300  
acgagattaa ctatggagct tggatggccc agatgtttctt gatccatgcc ttcactggca 360  
tggaggctga ggtcttactg gctatggctt ttgaccgtta tggatggccatc tggatccac 420  
tacattacgc aaccatcttgc acatccctag tggatgggg cattagcatg tgcattgtaa 480  
ttcgtcccgt tttacttaca cttccatgg tctatcttctt ctaccgccta ccctttgtc 540  
aggctcacat aatagcccat tcctactgtg agcacaatggg cattgcaaaa ttgtccctgtg 600  
gaaacattcg tatcaatggt atctatgggc tttttgtat ttctttctt gttctgaacc 660  
tggatgtcat tggatctcg tatgtttaca ttctccgtgc tggatggccatc tcccatcac 720  
atgatgtctca gctaaaagcc ctaaggcacgt gtcggatgtca tggatggatc atctgtgttt 780  
tctatatccc ttcagtttc tcttccttca ctcatcgatt tggacaccaa ataccagggtt 840  
acattcacat tcttggcc aatctctatt tgattatccc accctctctc aaccatca 900  
tttatgggg gaggacacaa cagattcggc agcgagtgct ctagttttt actaaaaat 960  
aagactcttca ccatgttatt ttact 985

<210> 16

<211> 311

<212> PRT

<213> Homo sapiens

<400> 16

Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu  
1 5 10 15

Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro  
20 25 30

Phe Cys Ser Val Tyr Leu Val Ala Leu Leu Gly Asn Ala Thr Ile Leu  
35 40 45

Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe  
50 55 60

Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Ala Thr Ser Val  
 65 70 75 80  
 Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr  
 85 90 95  
 Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met  
 100 105 110  
 Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Leu Val Leu Val  
 130 135 140  
 Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro  
 145 150 155 160  
 Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile  
 165 170 175  
 Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly  
 180 185 190  
 Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe  
 195 200 205  
 Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg  
 210 215 220  
 Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser  
 225 230 235 240  
 Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser  
 245 250 255  
 Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr  
 260 265 270  
 Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val  
 290 295 300  
 Leu Tyr Val Phe Thr Lys Lys  
 305 310

<210> 17  
 <211> 947  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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 atccccaggc tcgaaagactt ccacatgtgg atctccgggc ctttctgctc tgtttacctt 120  
 gtggctttgc tggcaatgc caccattctg ctatgtatca aggtagaaca gactctccgg 180  
 gagcccatgt tctacttcct ggcattctt tccactattg atttggccct ttctacaacc 240  
 tctgtgcctc gcatgctggg tatcttctgg tttgatgctc acgagattaa ctatggagct 300  
 tggatggccc agatgtttct gatccatgccc ttcactggca tggaggctga ggtctactg 360  
 gctatggctt ttgaccgtta tggccggtc tggatccac tacattacgc aaccatcttg 420  
 acatcccaag tggatgggg cattagcatg tgcattgtaa tccgtcccggt tttacttaca 480

cttcccatgg tctatcttat ctaccgccta ccctttgtc aggctcacat aatagccat 540  
tcctactgtg agcacatggg cattgcaaa ttgtcctgtg gaaacattcg tatcaatgg 600  
atctatgggc tttttgtagt ttccttctt gttctgaacc tggtgctcat tggcatctcg 660  
tatgtttaca ttctccgtgc tgtcttccgc ctcccatcac atgatgctca gctaaaagcc 720  
ctaaggacgt gtggcgctca tggtggagtc atctgtgttt tctatatccc ttcagtctc 780  
tcttcctta ctcatcgatt tggacaccaa ataccaggtt acattcacat tcttgggcc 840  
aatctctatt tgattatccc accctctctc aacccatca tttatggggt gaggaccaa 900  
cagattcgag aacgagtgc ctatgtttt actaaaaat aagacta 947

<210> 18  
<211> 311  
<212> PRT  
<213> Homo sapiens

<400> 18  
Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu  
1 5 10 15  
Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro  
20 25 30  
Phe Cys Ser Val Tyr Leu Val Ala Leu Leu Gly Asn Ala Thr Ile Leu  
35 40 45  
Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe  
50 55 60  
Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser Val  
65 70 75 80  
Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr  
85 90 95  
Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met  
100 105 110  
Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Val  
115 120 125  
Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Gln Val Leu Val  
130 135 140  
Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro  
145 150 155 160  
Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile  
165 170 175  
Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly  
180 185 190  
Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe  
195 200 205  
Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg  
210 215 220  
Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser  
225 230 235 240  
Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser  
245 250 255

Val	Phe	Ser	Phe	Leu	Thr	His	Arg	Phe	Gly	His	Gln	Ile	Pro	Gly	Tyr
260															
													270		

  

Ile	His	Ile	Leu	Val	Ala	Asn	Leu	Tyr	Leu	Ile	Ile	Pro	Pro	Ser	Leu
275															285

  

Asn	Pro	Ile	Ile	Tyr	Gly	Val	Arg	Thr	Lys	Gln	Ile	Arg	Glu	Arg	Val
290															300

  

Leu	Tyr	Val	Phe	Thr	Lys	Lys									
305															310

<210> 19  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
 gaaaaatgtt ttatcacaac aagagcatat ttcacccagt cacattttc ctcattggaa 60  
 tcccaggctc ggaagacttc cacatgtgga tctccggcc tttctgctct gttaccttg 120  
 cggctttgtc gggcaatgcc accattctgc tagtcatcaa ggtagaacag actctccggg 180  
 agcccatgtt ctacttcctg gccattctt ccactattga tttggccctt tctacaacct 240  
 ctgtgcctcg catgctgggt atcttctggt ttgatgctca cgagattaac tatggagett 300  
 gtgtggccca gatgttctg atccatgcct tcactggcat ggaggctgag gtcttactgg 360  
 ctatggctt tgaccgttat gtggccgtct gtgctccact acattacgca accatcttga 420  
 catcccaagt gttggggc attagcatgt gcattgtaat tcgtcccggtt ttacttacac 480  
 ttcccatggt ctatcttac taccgcctac cctttgtca ggctcacata atagcccatt 540  
 cctactgtga gcacatgggc attgcaaaat tgcctgtgg aaacattcgat atcaatggta 600  
 tctatgggc tttttagtt tctttctttt ttctgaacct ggtgctcatt ggcacatcgat 660  
 atgtttacat tctccgtct gtctccggcc tcccatcaca tgcgtctcag ctaaaagccc 720  
 taagcacgtg tggcgtctcat gttggagtca tctgtgtttt ctatatccct tcagtcttct 780  
 ctttccttac tcatcgattt ggacaccaaa taccaggta cattcacatt cttgttgcca 840  
 atctctattt gattatccca ccctctctca accccatcat ttatggggtg aggaccaa 900  
 agattcgaga acgagtgctc tatgtttta ctaaaaaata agact 945

<210> 20  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu  
 1 5 10 15

Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro  
 20 25 30

Phe Cys Ser Val Tyr Leu Ala Ala Leu Leu Gly Asn Ala Thr Ile Leu  
 35 40 45

Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe  
 50 55 60

Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser Val  
 65 70 75 80

Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr  
 85 90 95

Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met  
 15

100	105	110
Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Val		
115	120	125
Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Gln Val Leu Val		
130	135	140
Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro		
145	150	155
Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile		
165	170	175
Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly		
180	185	190
Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe		
195	200	205
Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg		
210	215	220
Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser		
225	230	235
Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser		
245	250	255
Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr		
260	265	270
Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu		
275	280	285
Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val		
290	295	300
Leu Tyr Val Phe Thr Lys Lys		
305	310	

<210> 21  
 <211> 1012  
 <212> DNA  
 <213> Homo sapiens

<400> 21

gcattcacaa gcaggatgtt cttcccaat gacacccagt ttcacccctc ctccttcctg 60  
 ttgctggga tcccaggact agaaacactt cacatctgga tcggcttcc cttctgtgct 120  
 gtgtacatga tcgcactcat agggacttc actattctac ttgtgatcaa gactgacagc 180  
 agcctacacc agcccatgtt ctacttcctg gccatgttgg ccaccactga tgtgggtctc 240  
 tcaacagcta ccattcctaa gatgcttgg atcttctgga tcaacactcag agggatcatc 300  
 tttgaagcct gcctcaccca gatgtttttt atccacaact tcacacttat ggagtcagca 360  
 gtccttgtgg caatggctt tgacagctat gtggccatct gcaatccact ccaatatacg 420  
 gccatcctca ccaacaagggt tgtttctgtt attggcttgc gtgtgtttgtt gagggcttta 480  
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 atccccacca cctactgtga gcacatgggt cttgctcatac tatcttgcgtc cagcatcaaa 600  
 atcaatatta tttatggttt atgtgccatt tgtaatctgg tgtttgcacat cacagtcatt 660  
 gcccctctt atgtgcataat tctttgtgtt gtttccgtc ttctactca tgagccccga 720  
 ctaaagtccc tcagcacatg tggttcacat gtgtgtgtaa tccttgcctt ctatacacca 780  
 gcccctttt cctttatgac tcattgcttt ggccgaaatg tgccccgcta tatccatata 840  
 ctccctagcca atctctatgt tgggtgcca ccaatgctca atcctgtcat atatggagtc 900

agaaccaagc agatctataa atgtgtaaag aaaatattat tgcaggaaca aggaatggaa 960  
aaggaagagt acctaataca tacgagggtc tgaatgcaat tttatgaaat tt 1012

<210> 22  
<211> 325  
<212> PRT  
<213> Homo sapiens

<400> 22  
Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu  
1 5 10 15  
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro  
20 25 30  
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu  
35 40 45  
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe  
50 55 60  
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile  
65 70 75 80  
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe  
85 90 95  
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met  
100 105 110  
Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile  
115 120 125  
Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser  
130 135 140  
Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro  
145 150 155 160  
Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile  
165 170 175  
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala  
180 185 190  
Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu  
195 200 205  
Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys  
210 215 220  
Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser  
225 230 235 240  
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala  
245 250 255  
Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr  
260 265 270  
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Pro Pro Met Leu  
275 280 285

Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val  
290 295 300

Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu  
305 310 315 320

Ile His Thr Arg Phe  
325

<210> 23  
<211> 1012  
<212> DNA  
<213> Homo sapiens

<400> 23  
gcattcacaa gcaggatgtt cttccaaat gacacccagt ttcacccctc ctccttcctg 60  
ttgctgggaa tcggcggact agaaacactt cacatctggc tcggctttcc cttctgtgt 120  
gtgtacatga tcggactcat agggacttc actattctac ttgtgtatcaa gactgacagc 180  
agcctacacc agcccatgtt ctacttcctg gccatgttgg ccaccactga tgtgggtctc 240  
tcaacagctc ccatccctaa gatgttggc atcttcgttgc tcaacactca agggatcatc 300  
tttgaagcct gcctcaccca gatgtttttt atccacaact tcacacttat ggagtcagca 360  
gtccttgcgttgc caatggcttgc tgacagctat gtggccatct gcaatccact ccaatatacg 420  
gccatccctca ccaacaagggt tgtttctgttgc attggcttgc gtgtgtttgtt gagggcttta 480  
attttcgatca ttccctctat acttcttata ttgcgttgc cttctgttgc gaatcatgtt 540  
attccccaca cctactgttgc gcacatgggt cttgttgcattc tatcttgcgttgc cagcatcaaa 600  
atcaatattttttt atgtgcattt tgtaatctatgt tggttgcacat cacagtattttttt 660  
gccctctctt atgtgcattat tctttctgttgc gttttccgttcttccactca tgaagcccgaa 720  
ctcaagtccc tcagcacatg tggttccatgt gtgtgtgttgc ttccctgttgc ttatacaccca 780  
gccctctttt cctttatgttgc tcattgttgc ttccctgttgc ttccctgttgc ttatacaccca 840  
ctccttagcca atctctatgt tggtgtgttgc ccaatgttgc atcctgttgc atatggagtc 900  
agaaccaaggc agatctataa atgtgtgttgc aaaaatattat tgcaaggaaaca aggaatggaa 960  
aaggaagagt acctaataaca tacgagggttgc tgaatgttgc ttatgttgc ttatgttgc 1012

<210> 24  
<211> 325  
<212> PRT  
<213> Homo sapiens

<400> 24  
Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu  
1 5 10 15

Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro  
20 25 30

Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu  
35 40 45

Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe  
50 55 60

Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile  
65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe  
85 90 95

Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met  
100 105 110

Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile  
115 120 125

Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser  
130 135 140

Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro  
145 150 155 160

Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile  
165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala  
180 185 190

Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu  
195 200 205

Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys  
210 215 220

Ala Val Phe Arg Leu Pro Thr His Glu Ala Arg Leu Lys Ser Leu Ser  
225 230 235 240

Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala  
245 250 255

Leu Phe Ser Phe Met Thr His Arg Phe Gly Arg Asn Val Pro Arg Tyr  
260 265 270

Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu  
275 280 285

Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val  
290 295 300

Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu  
305 310 315 320

Ile His Thr Arg Phe  
325

<210> 25

<211> 968

<212> DNA

<213> Homo sapiens

<400> 25

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catccatgcc caaatgctg gccatcttc ggttcaattc cactaccatc cagttgatg 300  
cttgtctgtc acagatgttt gccatccact ctttatctgg catggaatcc acagtgc 360  
tgccatggc ttttggccgc tatgtggcca tctgtcaccc actgcgc 420  
ttacgttgcc tcgtgtcacc aaaattgggtg tggctgtgt ggtgcggggg gctgcactga 480  
tgcacccct tcctgtcttc atcaaggcgc tgcccttctg cgcgtccaaat atcctttccc 540  
attcctactg cctacaccaa gatgtcatga agctggcctg tgatgatatac cgggtcaatg 600  
tcgtctatgg ctttatcgcc atcatctccg ccattggcct ggactcactt ctcatttc 660  
tctcatatct gcttatttctt aagactgtgt tgggcttgac acgtgaagcc caggccaagg 720  
catttggcac ttgcgtctct catgtgtgtg ctgtgttcat attctatgtatc ctttcattg 780  
gattgtccat ggtgcattgc ttttagcaagg ggcgtgactc tccgctgccc gtcattttgg 840

ccaatatcta tctgctgggtt cctcctgtgc tcaaccata tgcctatggg gtgaagacaa 900  
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aggtgtca 968

<210> 26  
<211> 318  
<212> PRT  
<213> Homo sapiens

<400> 26  
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
1 5 10 15  
Leu Ile Gly Leu Pro Gly Leu Glu Ala Gln Phe Trp Leu Ala Phe  
20 25 30  
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile  
35 40 45  
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile  
50 55 60  
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser  
65 70 75 80  
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln  
85 90 95  
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly  
100 105 110  
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
115 120 125  
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val  
130 135 140  
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala  
145 150 155 160  
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile  
165 170 175  
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys  
180 185 190  
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser  
195 200 205  
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile  
210 215 220  
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe  
225 230 235 240  
Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro  
245 250 255  
Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser  
260 265 270  
Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val  
20

275

280

285

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg  
290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
305 310 315

<210> 27  
<211> 969  
<212> DNA  
<213> Homo sapiens

<400> 27  
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cttattgtctg tgcttagttaa ctgtacaatc atctacattt tgccgactga gcacagcctg 180  
catgagccca tgtatataatt tctttgcattt ctttcaggca ttgacatcctt catctccacc 240  
tcatccatgc cccaaatgtt ggccatcttc tggttcaattt ccactaccat ccagtttgat 300  
gcttgtctgc tacagatgtt tgccatccac tccttatctg gcatggaatc cacagtgttg 360  
ctggccatgg ctttgaccg ctatgtggcc atctgtcacc cactgcgcac tgccacagta 420  
cttacgttgc ctgtgttgc cccaaatttgtt gtggctgttgg tgggtgcgggg ggctgcactg 480  
atggcaccctt ttcctgttgc catcaagcag ctgccttgc tggctccaa ttcctttcc 540  
catttcctact gcccacacca agatgtcatg aagctggcctt gtgatgatat ccgggtcaat 600  
gtcgtctatgt gccttatctgtt catcatctcc gccattggcc tggactcaact ttcatctcc 660  
tttcataatc tggcttattttt taagactgttgg tgggtgttgc cactgtgaagc ccaggccaa 720  
gcatttggca cttgcgttgc tcatgtgtgtt gctgtgttca tattctatgtt acctttcattt 780  
ggattgttcca tgggtgttgc cttagcaag cggcgttactt ctccactgccc cgtcatcttgc 840  
gccaatatctt atctgtgttgc ttccatgttgc cccacacacgc ttcagagcccc 900  
aaggagatttgc gacagcgttgc ctttcgttgc ttccatgttgc cccacacacgc ttcagagcccc 960  
taggtgttca 969

<210> 28  
<211> 318  
<212> PRT  
<213> Homo sapiens

<400> 28  
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
1 5 10 15

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe  
20 25 30

Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile  
35 40 45

Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile  
50 55 60

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser  
65 70 75 80

Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln  
85 90 95

Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly  
100 105 110

Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
115 120 125

Ile	Cys	His	Pro	Leu	Arg	His	Ala	Thr	Val	Leu	Thr	Leu	Pro	Arg	Val
130				135					140						
Thr	Lys	Ile	Gly	Val	Ala	Ala	Val	Val	Arg	Gly	Ala	Ala	Leu	Met	Ala
145				150					155				160		
Pro	Leu	Pro	Val	Phe	Ile	Lys	Gln	Leu	Pro	Phe	Cys	Arg	Ser	Asn	Ile
	165				170					175					
Leu	Ser	His	Ser	Tyr	Cys	Pro	His	Gln	Asp	Val	Met	Lys	Leu	Ala	Cys
	180				185					190					
Asp	Asp	Ile	Arg	Val	Asn	Val	Val	Tyr	Gly	Leu	Ile	Val	Ile	Ile	Ser
	195				200					205					
Ala	Ile	Gly	Leu	Asp	Ser	Leu	Leu	Ile	Ser	Phe	Ser	Tyr	Leu	Leu	Ile
	210				215				220						
Leu	Lys	Thr	Val	Leu	Gly	Leu	Thr	Arg	Glu	Ala	Gln	Ala	Lys	Ala	Phe
	225				230				235				240		
Gly	Thr	Cys	Val	Ser	His	Val	Cys	Ala	Val	Phe	Ile	Phe	Tyr	Val	Pro
	245				250					255					
Phe	Ile	Gly	Leu	Ser	Met	Val	His	Arg	Phe	Ser	Lys	Arg	Arg	Asp	Ser
	260				265					270					
Pro	Leu	Pro	Val	Ile	Leu	Ala	Asn	Ile	Tyr	Leu	Leu	Val	Pro	Pro	Val
	275				280					285					
Leu	Asn	Pro	Ile	Val	Tyr	Gly	Val	Lys	Thr	Lys	Glu	Ile	Arg	Gln	Arg
	290				295				300						
Ile	Leu	Arg	Leu	Phe	His	Val	Ala	Thr	His	Ala	Ser	Glu	Pro		
	305				310				315						

<210> 29  
 <211> 968  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
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 ctattgctg tgcttaggtaa cttgacaatc atctacattg tgcggactga gcacagcctg 180  
 catgagccca tgtatataatt tctttgcattt ctttcaggca ttgacatctt catctccacc 240  
 tcatccatgc cccaaatgct ggccatcttc tggccaattt ccactaccat ccagtttgat 300  
 gcttgcgtgc tacagatgtt tgccatccac tccttatctg gcatggaatc cacagtgcgtg 360  
 ctggccatgg ctttgaccg ctatgtggcc atctgtcacc cactgcgc 420  
 ctacgttgc ctcgtgtcac caaaattgggt gtggctgctg tggcgcccc ggctgcactg 480  
 atggcacccccc ttccctgtctt catcaagcag ctgccttctt gcccgtccaa tattttcc 540  
 cattcctact gcccacacca agatgtcatg aagctggcct gtgatgatat ccgggtcaat 600  
 gtcgtctatg gccttacatgtt catcatctcc gccattggcc tggactcaat tctcatctcc 660  
 ttctcatatc tgcttattct taagactgtt tggcgatcc cactgtggcc cacgtgaagc ccaggccaa 720  
 gcatttggca cttgcgtctc tcatgtgtgt gctgtgttca tattctatgtt acctttcatt 780  
 ggattgttca tggtgatcg cttagcaag cggcgactt ctccactgccc cgtcatctt 840  
 gccaatatctt atctgtgtt tccctgttgc ctcaacccaa ttgtctatgg agtgaagaca 900  
 aaggagattt gacagcgcat cttcgactt ttccatgtgg ccacacacgc ttcagagccc 960  
 taggtgtt 968

<210> 30  
<211> 318  
<212> PRT  
<213> Homo sapiens

<400> 30  
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
1 5 10 15  
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe  
20 25 30  
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile  
35 40 45  
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile  
50 55 60  
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser  
65 70 75 80  
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln  
85 90 95  
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly  
100 105 110  
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
115 120 125  
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val  
130 135 140  
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala  
145 150 155 160  
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile  
165 170 175  
Leu Ser His Ser Tyr Cys Pro His Gln Asp Val Met Lys Leu Ala Cys  
180 185 190  
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser  
195 200 205  
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile  
210 215 220  
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe  
225 230 235 240  
Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro  
245 250 255  
Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser  
260 265 270  
Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val  
275 280 285  
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg  
290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
305 310 315

<210> 31  
<211> 980  
<212> DNA  
<213> Homo sapiens

<400> 31  
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gtatcccagg actgcaatct tcacatctt ggctggctat ctcactgagt gccatgtaca 120  
tcacagccct gtttagaaac accctcatcg tgactgcaat ctggatggat tccactcggc 180  
atgagcccat gtattgtctt ctgtgtgttc tggctgtgt ggacattgtt atggcctcct 240  
ccgtggtacc caagatggtg agcatcttct gctcgggaga cagctccatc agcttagtg 300  
cttgtttcac tcagatgttt ttgttccact tagccacagc tggagacg gggctgctgc 360  
tgaccatggc ttttgaccgc tatgttagcca tctgcaagcc tctacactac aagagaattc 420  
tcacgcctca agtgtatgtc ggaatgagta tggccgtcac catcagact gtcacattca 480  
tgactccact gagttggatg atgaatcatc taccttctg tggctccaat gtgggtgtcc 540  
actcctactg taagcacata gctttggcca ggtagcatg tgctgaccgg gtgcccagca 600  
gtctctacag tctgattggc tccctcttta tgggtggctc tggatgtggcc ttcattgctg 660  
cctcctataat cttaattctc agggcagttat ttgatctctc ctcaaagact gctcagttga 720  
aagcattaag cacatgtggc tcccatgtgg gggttatggc tttgtactat ctacctggga 780  
tgcatccat ctatgcggcc tgggtggggc aggatatagt gcccattgcac acccaagtgc 840  
tcttagctga cctgtacgtg atcatcccaag ccacttaaa tcccatcatc tatggcatga 900  
ggaccaaaca attgctggag ggaatatgga gttatctgat gcacttcctc tttgaccact 960  
ccaacctggg ttcatgaaca 980

<210> 32  
<211> 324  
<212> PRT  
<213> Homo sapiens

<400> 32  
Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
1 5 10 15

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
20 25 30

Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu  
35 40 45

Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
50 55 60

Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
65 70 75 80

Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
85 90 95

Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
100 105 110

Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
115 120 125

Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
130 135 140

Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met  
24

145	150	155	160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn			
165	170	175	
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala			
180	185	190	
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser			
195	200	205	
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu			
210	215	220	
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys			
225	230	235	240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr			
245	250	255	
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile			
260	265	270	
Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile			
275	280	285	
Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu			
290	295	300	
Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His Ser			
305	310	315	320
Asn Leu Gly Ser			

<210> 33  
 <211> 985  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
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 ggttatccca ggactgcaat cttcacatct ttggctggct atctcactga gtgcacatgt 120  
 catcatagcc ctgttaggaa acaccatcat cgtgactgca atctggatgg attccactcg 180  
 gcatgagccc atgtattgct ttctgtgtgt tctggctgct gtggacattg ttatggcctc 240  
 ctcggtgtta cccaagatgg tgagcatctt ctgctcagga gacagctcaa tcagctttag 300  
 tgcttgtttc actcagatgt tttttgtcca cttagccaca gctgtggaga cggggctgct 360  
 gctgaccatg gcttttgacc gctatgttagc catctgcaag cctctacact acaagagaat 420  
 tctcacgcct caagtgatgc tggaaatgag tatggccatc accatcagag ctatcatagc 480  
 cataactcca ctgagttgga tggtgagtca tctacccctc tggctcata atgtggttgt 540  
 ccactcctac tgtgagcaca tagctttggc caggtagca tggctgacc ccgtgcccag 600  
 cagtctctac agtctgattt gttccctctct tatgggtggc tctgatgtgg ctttattgc 660  
 tgcctcctat atcttaattt tcaaggcagt atttggcttc tcctcaaaga ctgctcagtt 720  
 gaaagcatttta agcacatgtg gtcctccatgt gggggatgt gctttgtact atctacccatgg 780  
 gatggcatcc atctatgcgg cctgggtggc gcaggatgtt gtcgccttgc acacccaaatgt 840  
 cctgcttagct gacctgtacg tgatcatccc agccacccatca aatcccatca tctatggcat 900  
 gaggacccaaa caactgcggg agagaatatg gagttatctg atgcacatgtcc tctttgacca 960  
 ttccaaacccatgg ggttcatgaa caca 985

<210> 34  
 <211> 324

<212> PRT

<213> Homo sapiens

<400> 34

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
1 5 10 15

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
20 25 30

Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Ile  
35 40 45

Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
50 55 60

Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
65 70 75 80

Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
85 90 95

Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
100 105 110

Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
115 120 125

Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
130 135 140

Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile  
145 150 155 160

Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn  
165 170 175

Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala  
180 185 190

Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
195 200 205

Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
210 215 220

Ile Leu Lys Ala Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys  
225 230 235 240

Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
245 250 255

Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val  
260 265 270

Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
275 280 285

Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
290 295 300

Arg Glu Arg Ile Trp Ser Tyr Leu Met His Val Leu Phe Asp His Ser  
305 310 315 320

Asn Leu Gly Ser

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<210> 35
<211> 985
<212> DNA
<213> Homo sapiens

<400> 35
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catcacagcc ctgttaggaa acaccatcat cgtgactgca atctggatgg attccactcg 180
gcatgagccc atgtattgct ttctgtgtgt tctggctgct gtggacattt ttatggccct 240
ctcgggttta cccaaatgg tgagcatctt ctgctcagga gacagctcaa tcagctttag 300
tgcttgtttc actcagatgt tttttgtcca cttagccaca gctgtggaga cggggctgct 360
gctgaccatg gcttttgacc gctatgttagc catctgcaag cctctacact acaagagaat 420
tctcacgcct caagtgtatgc tggaaatgag tatggccatc accatcagag ctatcatagc 480
cataactcca ctgagtttga tggtgagtca tctaccttc tggcttca atgtggttgt 540
ccactccctac tggtagcaca tagcttggc caggttagca tggctgacc ccgtgcccag 600
cagtcctctac agtctgattt gttccctctt tatgggtggc tctgatgtgg ctttcattgc 660
tgcctccat atcttaattc tcagggcagt atttgatctc tcccaaaga ctgctcagtt 720
gaaagcatta agcacatgt gctcccatgt gggggttatg gctttgtact atctacctgg 780
gatggcatcc atctatgcgg cttgggtggc gcaggatata gtgccttgc acacccaagt 840
gctgttagct gacctgtacg tgatcatccc agccacttta aatcccatca tctatggcat 900
gaggacccaaa caattgtgg agggaaatatg gagttatctg atgcacttcc tctttgacca 960
ctccaaacctg ggttcatgaa caca 985
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<210> 36
<211> 324
<212> PRT
<213> Homo sapiens

<400> 36
Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
 1           5           10          15

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
 20          25          30

Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Ile
 35          40          45

Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
 50          55          60

Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
 65          70          75          80

Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
 85          90          95

Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
100          105         110

Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
115          120         125

Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
130          135         140

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Met	Leu	Gly	Met	Ser	Met	Ala	Ile	Thr	Ile	Arg	Ala	Ile	Ile	Ala	Ile
145					150					155				160	
Thr	Pro	Leu	Ser	Trp	Met	Val	Ser	His	Leu	Pro	Phe	Cys	Gly	Ser	Asn
					165				170				175		
Val	Val	Val	His	Ser	Tyr	Cys	Glu	His	Ile	Ala	Leu	Ala	Arg	Leu	Ala
					180			185				190			
Cys	Ala	Asp	Pro	Val	Pro	Ser	Ser	Leu	Tyr	Ser	Leu	Ile	Gly	Ser	Ser
					195			200			205				
Leu	Met	Val	Gly	Ser	Asp	Val	Ala	Phe	Ile	Ala	Ala	Ser	Tyr	Ile	Leu
					210			215			220				
Ile	Leu	Arg	Ala	Val	Phe	Asp	Leu	Ser	Ser	Lys	Thr	Ala	Gln	Leu	Lys
					225			230		235			240		
Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Val	Gly	Val	Met	Ala	Leu	Tyr	Tyr
					245			250			255				
Leu	Pro	Gly	Met	Ala	Ser	Ile	Tyr	Ala	Ala	Trp	Leu	Gly	Gln	Asp	Ile
					260			265			270				
Val	Pro	Leu	His	Thr	Gln	Val	Leu	Leu	Ala	Asp	Leu	Tyr	Val	Ile	Ile
					275			280			285				
Pro	Ala	Thr	Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Met	Arg	Thr	Lys	Gln	Leu
					290			295			300				
Leu	Glu	Gly	Ile	Trp	Ser	Tyr	Leu	Met	His	Phe	Leu	Phe	Asp	His	Ser
					305			310			315			320	
Asn	Leu	Gly	Ser												

<210> 37  
<211> 960  
<212> DNA  
<213> Homo sapiens

<400> 37  
gccccatgctca cttttcataa tgtctgctca gtacccagct ccttctggct cactggcattc 60  
ccaggggctgg agtccctaca cgtctggctc tccatccccct ttggctccat gtacctggtg 120  
gtctgtggtg ggaatgtgac catcctggct gtggtaaaga tagaaacgcag cctgcaccag 180  
cccatgtact ttttcttgtg catgttggct gccattgacc tggttctgtc tacttccact 240  
atacccaaac ttctggaaat cttctggttc ggtgcttgtg acattggctt ggacgcctgc 300  
ttggggccaaa tggcccttat ccactgcttt gccactgttg agtcaggcat cttcccttgcc 360  
atggcttttg atcgctacgt ggccatctgc aaccactac gtcatagcat ggtgctact 420  
tatacagtgg tgggtcgttt ggggcttgtt tctctctcc ggggtgttct ctacattgga 480  
cctctgcctc tgatgatccg cctgcggctg cccctttata aaacccatgt tatctccac 540  
tctctactgtg agcacatggc tggatgttgc ttgacatgtg ggcacagcag ggtcaataat 600  
gtctatgggc tgagcatcg ctttctggtg ttgatctgg actcagtgc tattgctgca 660  
tctctatgtg tgattttcg ggccgtgatg gggtagcca ctccctgagcc taggttaaa 720  
accctgggaa catgcgttc tcacctctgt gccatctga tcttttatgt tcccattgct 780  
gtttcttccc tgattcaccg atttggtcag tggatgtgc ctcaggatcca cactctgctg 840  
gccaacttct atctccat tcctccaatc ctcaatccca ttgtctatgc tggatgcacc 900  
aagcagatcc gagagagcct tctccaaata ccaaggatag aatgaagat tagatgatta 960

<210> 38  
<211> 317

<212> PRT

<213> Homo sapiens

<400> 38

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
1 5 10 15

Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
20 25 30

Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
35 40 45

Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
50 55 60

Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
65 70 75 80

Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
85 90 95

Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
100 105 110

Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
115 120 125

Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
130 135 140

Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
145 150 155 160

Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
180 185 190

Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu  
195 200 205

Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile  
210 215 220

Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr  
225 230 235 240

Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val  
245 250 255

Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro  
260 265 270

Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro  
275 280 285

Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu  
290 295 300

Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg  
305 310 315

<210> 39  
<211> 997  
<212> DNA  
<213> Homo sapiens

<400> 39  
agccatgctc actttcata atgtctgctc agtacccagc tccttctggc tcactggcat 60  
cccaggcgtc gagtcctac acgtctggc ctccatcccc tttggctcca tgtacctgg 120  
ggctgtggtg gggaaatgtga ccattcctgac tggtaaaag atagaacgca gcctgcacca 180  
gcccatgtac ttttcttgc gcatgttgc tgccattgac ctggttctgt ctacttccac 240  
tatacccaa cttctggaa ttttctgggtt cgggtctgtt gacattggcc tggatgcctg 300  
cttggccaa atgttcctta tccactgctt tgccactggtt gaggcaggca tcttccttgc 360  
catggctttt gatcgctatg tggccatctg caacccacta cgtcatagca tggtgctcac 420  
ttatacagtg gtgggtcggtt tggggcttgc ttcttcctc cgggggtgtc tctacattgg 480  
acccctgcctt ctgatgatcc gcctgcgggtt gcccctttat aaaacccatg ttatctccca 540  
ctcctactgtt gggccatgg ctgttagttgc ctgtgacatgtt ggcgacagca gggtaataa 600  
tgtctatggg ctgagcatcg gctttctgtt gttgatcctg gactcagtgg ctattgctgc 660  
atccatgttgc atgatttca gggccgtgtat ggggttagcc acccctgaggc ctggcttaa 720  
aaccctgggg acatgcgtt ctcacctctg tgccatcctg atctttatg ttccattgc 780  
tggggccatcc tatcttcctca ttccctccaaat cctcaatccc attgtctatg ctgttcgcac 840  
caagcagatc cgagagaggc ttctccaaat accaaggata gaaatgaaga ttagatgatt 900  
actatttctc tctctctcaa ataagctcat ggagaag 997

<210> 40  
<211> 317  
<212> PRT  
<213> Homo sapiens

<400> 40  
Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
1 5 10 15

Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
20 25 30

Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
35 40 45

Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
50 55 60

Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
65 70 75 80

Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
85 90 95

Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
100 105 110

Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
115 120 125

Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
130 135 140

Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
145 150 155 160

Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
180 185 190

Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu  
195 200 205

Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile  
210 215 220

Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr  
225 230 235 240

Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val  
245 250 255

Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro  
260 265 270

Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro  
275 280 285

Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu  
290 295 300

Arg Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg  
305 310 315

<210> 41  
<211> 997  
<212> DNA  
<213> Homo sapiens

<400> 41

agccatgctc acttttcata atgtctgctc agtacccagc tccttctggc tcactggcat 60  
cccaaggctg gagtcctac acgtctggct ctccatcccc ttggctcca tgtacctgg 120  
ggctgtgggt gggaatgtga ccatacggc tggtaaaag atagaacgca gcctgcacca 180  
gccccatgtac tttttcttgc gcatgttggc tgccattgac ctggttctgt ctacttccac 240  
tatacccaa cttctggaa tcttctgggt cggtgctgt gacattggcc tggatgcctg 300  
cttggcccaa atgttctta tccactgct tgccactgtt gagtcaggca tcttccttgc 360  
catggctttt gatcgatcg tggccatctg caaccacta cgtcatagca tggtgctcac 420  
ttatacagtgc tggggcttgc tggggcttgc ttctctcctc cgggggtgtc tctacattgg 480  
acctctgcct ctgatgatcc gcctgcgggt gcccctttat aaaacccatg ttatctccca 540  
ctcctactgt gaggcacatgg ctgttagttgc cttgacatgt ggcgcacagaca gggtaataa 600  
tgtctatggg ctgagacatcg gctttctggt gttgatcctg gactcagttgg ctattgctgc 660  
atccatgttgc atgattttca gggccgtat ggggttagcc actcctgagg ctaggcttaa 720  
aaccctgggg acatgcgtt ctcacatctg tgccatcctg atctttatg ttcccattgc 780  
tggttcttcc ctgattcacc gatttggatca gtgtgtgcct cctccagtc acactctgt 840  
ggccaacttc tatctcctca ttccctcaat cctcaatccc attgtctatg ctgttcgcac 900  
caagcagatc cgagagaggc ttctccaaat accaaggata gaaatgaaga ttagatgatt 960  
actatttct tctctctcaa ataagctcat ggagaag 997

<210> 42  
<211> 317  
<212> PRT  
<213> Homo sapiens

<400> 42

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu

1	5	10	15												
Thr	Gly	Ile	Pro	Gly	Leu	Glu	Ser	Leu	His	Val	Trp	Leu	Ser	Ile	Pro
				20				25						30	
Phe	Gly	Ser	Met	Tyr	Leu	Val	Ala	Val	Val	Gly	Asn	Val	Thr	Ile	Leu
			35				40					45			
Ala	Val	Val	Lys	Ile	Glu	Arg	Ser	Leu	His	Gln	Pro	Met	Tyr	Phe	Phe
			50				55				60				
Leu	Cys	Met	Leu	Ala	Ala	Ile	Asp	Leu	Val	Leu	Ser	Thr	Ser	Thr	Ile
			65			70				75				80	
Pro	Lys	Leu	Leu	Gly	Ile	Phe	Trp	Phe	Gly	Ala	Cys	Asp	Ile	Gly	Leu
			85				90						95		
Asp	Ala	Cys	Leu	Gly	Gln	Met	Phe	Leu	Ile	His	Cys	Phe	Ala	Thr	Val
			100				105						110		
Glu	Ser	Gly	Ile	Phe	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile
			115				120					125			
Cys	Asn	Pro	Leu	Arg	His	Ser	Met	Val	Leu	Thr	Tyr	Thr	Val	Val	Gly
			130			135				140					
Arg	Leu	Gly	Leu	Val	Ser	Leu	Leu	Arg	Gly	Val	Leu	Tyr	Ile	Gly	Pro
			145				150			155			160		
Leu	Pro	Leu	Met	Ile	Arg	Leu	Arg	Leu	Pro	Leu	Tyr	Lys	Thr	His	Val
			165				170					175			
Ile	Ser	His	Ser	Tyr	Cys	Glu	His	Met	Ala	Val	Val	Ala	Leu	Thr	Cys
			180				185					190			
Gly	Asp	Ser	Gly	Val	Asn	Asn	Val	Tyr	Gly	Leu	Ser	Ile	Gly	Phe	Leu
			195			200					205				
Val	Leu	Ile	Leu	Asp	Ser	Val	Ala	Ile	Ala	Ala	Ser	Tyr	Val	Met	Ile
			210			215					220				
Phe	Arg	Ala	Val	Met	Gly	Leu	Ala	Thr	Pro	Glu	Ala	Arg	Leu	Lys	Thr
			225				230			235			240		
Leu	Gly	Thr	Cys	Ala	Ser	His	Leu	Cys	Ala	Ile	Leu	Ile	Phe	Tyr	Ile
			245				250					255			
Pro	Ile	Ala	Val	Ser	Ser	Leu	Ile	His	Arg	Phe	Gly	Gln	Cys	Val	Pro
			260				265					270			
Pro	Pro	Val	His	Thr	Leu	Leu	Ala	Asn	Phe	Tyr	Leu	Leu	Ile	Pro	Pro
			275				280					285			
Ile	Leu	Asn	Pro	Ile	Val	Tyr	Ala	Val	Arg	Thr	Lys	Gln	Ile	Arg	Glu
			290				295				300				
Arg	Leu	Leu	Gln	Ile	Pro	Arg	Ile	Glu	Met	Lys	Ile	Arg			
			305			310				315					

<210> 43  
 <211> 387  
 <212> PRT

<213> Homo sapiens

<400> 43

Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys  
1 5 10 15

Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro  
20 25 30

Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala  
35 40 45

Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile  
50 55 60

Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu  
65 70 75 80

Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly  
85 90 95

Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln  
100 105 110

Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg  
115 120 125

Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala  
130 135 140

Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val  
145 150 155 160

His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val  
165 170 175

Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met  
180 185 190

Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser  
195 200 205

Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala  
210 215 220

Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe  
225 230 235 240

Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp  
245 250 255

Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val  
260 265 270

Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
275 280 285

Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe  
290 295 300

Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu  
305 310 315 320

Pro	Asp	Asn	Asn	Arg	Ser	Thr	Ser	Val	Glu	Leu	Thr	Gly	Asp	Pro	Asn
									325	330					335
Lys	Thr	Arg	Gly	Ala	Pro	Glu	Ala	Leu	Met	Ala	Asn	Ser	Gly	Glu	Pro
									340	345					350
Trp	Ser	Pro	Ser	Tyr	Leu	Gly	Pro	Thr	Ser	Asn	Asn	His	Ser	Lys	Lys
									355	360					365
Gly	His	Cys	His	Gln	Glu	Pro	Ala	Ser	Leu	Glu	Lys	Gln	Leu	Gly	Cys
									370	375					380
Cys	Ile	Glu													
									385						

<210>	44														
<211>	360														
<212>	PRT														
<213>	Mus	musculus													
<400>	44														
Met	Ser	Lys	Ser	Asp	His	Phe	Leu	Val	Ile	Asn	Gly	Lys	Asn	Cys	Cys
									1	5					15
Val	Phe	Arg	Asp	Glu	Asn	Ile	Ala	Lys	Val	Leu	Pro	Pro	Val	Leu	Gly
									20	25					30
Leu	Glu	Phe	Val	Phe	Gly	Leu	Leu	Gly	Asn	Gly	Leu	Ala	Leu	Trp	Ile
									35	40					45
Phe	Cys	Phe	His	Ile	Lys	Ser	Trp	Lys	Ser	Ser	Arg	Ile	Phe	Leu	Phe
									50	55					60
Asn	Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu	Ile	Ile	Cys	Leu	Pro	Phe	Leu
									65	70					80
Thr	Asp	Asn	Tyr	Val	His	Asn	Trp	Asp	Trp	Arg	Phe	Gly	Gly	Ile	Pro
									85	90					95
Cys	Arg	Val	Met	Leu	Phe	Met	Leu	Ala	Met	Asn	Arg	Gln	Gly	Ser	Ile
									100	105					110
Ile	Phe	Leu	Thr	Val	Val	Ala	Val	Asp	Arg	Tyr	Phe	Arg	Val	Val	His
									115	120					125
Pro	His	His	Phe	Leu	Asn	Lys	Ile	Ser	Asn	Arg	Thr	Ala	Ala	Ile	Ile
									130	135					140
Ser	Cys	Phe	Leu	Trp	Gly	Leu	Thr	Ile	Gly	Leu	Thr	Val	His	Leu	Leu
									145	150					160
Tyr	Thr	Asn	Met	Met	Thr	Lys	Asn	Gly	Glu	Ala	Tyr	Leu	Cys	Ser	Ser
									165	170					175
Phe	Ser	Ile	Cys	Tyr	Asn	Phe	Arg	Trp	His	Asp	Ala	Met	Phe	Leu	Leu
									180	185					190
Glu	Phe	Phe	Leu	Pro	Leu	Ala	Ile	Ile	Leu	Phe	Cys	Ser	Gly	Arg	Ile
									195	200					205
Ile	Trp	Ser	Leu	Arg	Gln	Arg	Gln	Met	Asp	Arg	His	Ala	Lys	Ile	Lys
									210	215					220

Arg Ala Ile Asn Phe Ile Met Val Val Ala Ile Val Phe Ile Ile Cys  
225 230 235 240

Phe Leu Pro Ser Val Ala Val Arg Ile Arg Ile Phe Trp Leu Leu Tyr  
245 250 255

Lys Tyr Asn Val Arg Asn Cys Asp Ile Tyr Ser Ser Val Asp Leu Ala  
260 265 270

Phe Phe Thr Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro  
275 280 285

Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe Phe Ser Thr  
290 295 300

Cys Ile Asn Arg Cys Leu Arg Lys Lys Thr Leu Gly Glu Pro Asp Asn  
305 310 315 320

Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Ser Thr Thr Arg  
325 330 335

Ser Ile Pro Gly Ala Leu Met Ala Asp Pro Ser Glu Pro Gly Ser Pro  
340 345 350

Pro Tyr Leu Ala Ser Thr Ser Arg  
355 360

<210> 45  
<211> 319  
<212> PRT  
<213> Mus musculus

<400> 45  
Met Glu His Thr Asn Cys Ser Ala Ala Ser Thr Val Val Glu Thr Ala  
1 5 10 15

Val Gly Thr Met Leu Thr Leu Glu Cys Val Leu Gly Leu Met Gly Asn  
20 25 30

Ala Val Ala Leu Trp Thr Phe Phe Tyr Arg Leu Lys Val Trp Lys Pro  
35 40 45

Tyr Ala Val Tyr Leu Phe Asn Leu Val Val Ala Asp Leu Leu Ala  
50 55 60

Thr Ser Val Pro Phe Phe Ala Ala Phe Tyr Leu Lys Gly Lys Thr Trp  
65 70 75 80

Lys Leu Gly His Met Pro Cys Gln Leu Leu Leu Phe Leu Leu Ala Phe  
85 90 95

Ser Cys Gly Val Gly Val Ala Phe Leu Met Thr Val Ala Leu Asp Arg  
100 105 110

Tyr Leu His Val Val His Pro Arg Leu Arg Val Asn Leu Leu Ser Leu  
115 120 125

Arg Ala Ala Trp Gly Ile Ser Ser Leu Ile Trp Leu Leu Met Val Val  
130 135 140

Leu Thr Pro Gln Asn Leu Leu Thr Cys Arg Thr Thr Gln Asn Ser Thr  
35

145	150	155	160
Glu Cys Pro Ser Phe Tyr Pro Thr Gly Gly Thr Lys Ala Ile Ala Thr			
165	170	175	
Cys Gln Glu Val Leu Phe Phe Leu Gln Val Leu Leu Pro Phe Gly Leu			
180	185	190	
Ile Ser Phe Cys Asn Ser Gly Leu Ile Arg Thr Leu Gln Lys Arg Leu			
195	200	205	
Ser Glu Ser Asp Lys Gln Pro Thr Ile Arg Arg Ala Arg Val Leu Val			
210	215	220	
Ala Ile Met Leu Leu Leu Phe Gly Leu Cys Phe Leu Pro Ser Val Leu			
225	230	235	240
Thr Arg Val Leu Val His Ile Phe Gln Glu Phe Lys Ser Cys Ser Val			
245	250	255	
Gln Gln Ala Ile Met Arg Ala Ser Asp Ile Ala Gly Ser Leu Thr Cys			
260	265	270	
Leu His Ser Thr Leu Ser Pro Ala Ile Tyr Cys Phe Ser Asn Pro Ala			
275	280	285	
Phe Thr His Ser Tyr Arg Lys Val Leu Lys Ser Leu Arg Gly Arg Arg			
290	295	300	
Lys Ala Ala Glu Ser Pro Ser Asp Asn Leu Arg Asp Ser Tyr Ser			
305	310	315	
<210> 46			
<211> 362			
<212> PRT			
<213> Gallus gallus			
<400> 46			
Met Thr Glu Ala Leu Ile Ser Ala Ala Leu Asn Gly Thr Gln Pro Glu			
1	5	10	15
Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Thr Thr Lys Cys Ser			
20	25	30	
Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile			
35	40	45	
Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met			
50	55	60	
Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe			
65	70	75	80
Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu			
85	90	95	
Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met			
100	105	110	
Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile			
115	120	125	

Leu	Phe	Leu	Thr	Cys	Ile	Ser	Val	His	Arg	Tyr	Thr	Gly	Val	Val	His
130															140
Pro	Leu	Lys	Ser	Leu	Gly	Arg	Leu	Lys	Lys	Asn	Ala	Val	Tyr	Val	
145															160
Ser	Ser	Leu	Val	Trp	Ala	Leu	Val	Val	Ala	Val	Ile	Ala	Pro	Ile	Leu
															175
Phe	Tyr	Ser	Gly	Thr	Gly	Val	Arg	Arg	Asn	Lys	Thr	Ile	Thr	Cys	Tyr
															190
Asp	Thr	Thr	Ala	Asp	Glu	Tyr	Leu	Arg	Ser	Tyr	Phe	Val	Tyr	Ser	Met
															195
															200
															205
Cys	Thr	Thr	Val	Phe	Met	Phe	Cys	Ile	Pro	Phe	Ile	Val	Ile	Leu	Gly
															210
															215
															220
Cys	Tyr	Gly	Leu	Ile	Val	Lys	Ala	Leu	Ile	Tyr	Lys	Asp	Leu	Asp	Asn
															225
															230
															235
															240
Ser	Pro	Leu	Arg	Arg	Lys	Ser	Ile	Tyr	Leu	Val	Ile	Ile	Val	Leu	Thr
															245
															250
															255
Val	Phe	Ala	Val	Ser	Tyr	Leu	Pro	Phe	His	Val	Met	Lys	Thr	Leu	Asn
															260
															265
															270
Leu	Arg	Ala	Arg	Leu	Asp	Phe	Gln	Thr	Pro	Gln	Met	Cys	Ala	Phe	Asn
															275
															280
															285
Asp	Lys	Val	Tyr	Ala	Thr	Tyr	Gln	Val	Thr	Arg	Gly	Leu	Ala	Ser	Leu
															290
															295
															300
Asn	Ser	Cys	Val	Asp	Pro	Ile	Leu	Tyr	Phe	Leu	Ala	Gly	Asp	Thr	Phe
															305
															310
															315
															320
Arg	Arg	Arg	Leu	Ser	Arg	Ala	Thr	Arg	Lys	Ser	Ser	Arg	Arg	Ser	Glu
															325
															330
															335
Pro	Asn	Val	Gln	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Asn	Ile	Leu	Thr
															340
															345
															350
Glu	Tyr	Lys	Gln	Asn	Gly	Asp	Thr	Ser	Leu						
															355
															360

<210> 47

<211> 362

<212> PRT

<213> *Meleagris gallopavo*

<400> 47

Met	Thr	Glu	Ala	Leu	Ile	Ser	Ala	Ala	Leu	Asn	Gly	Thr	Gln	Pro	Glu
1															15

Leu	Leu	Ala	Gly	Gly	Trp	Ala	Ala	Gly	Asn	Ala	Ser	Thr	Lys	Cys	Ser
															20
															25
															30

Leu	Thr	Lys	Thr	Gly	Phe	Gln	Phe	Tyr	Tyr	Leu	Pro	Thr	Val	Tyr	Ile
															35
															40
															45

Leu	Val	Phe	Ile	Thr	Gly	Phe	Leu	Gly	Asn	Ser	Val	Ala	Ile	Trp	Met
															50
															55
															60

Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe  
 65 70 75 80  
 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu  
 85 90 95  
 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met  
 100 105 110  
 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile  
 115 120 125  
 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His  
 130 135 140  
 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val  
 145 150 155 160  
 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu  
 165 170 175  
 Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr  
 180 185 190  
 Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met  
 195 200 205  
 Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly  
 210 215 220  
 Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn  
 225 230 235 240  
 Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr  
 245 250 255  
 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn  
 260 265 270  
 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn  
 275 280 285  
 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu  
 290 295 300  
 Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe  
 305 310 315 320  
 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu  
 325 330 335  
 Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr  
 340 345 350  
 Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu  
 355 360

<210> 48  
 <211> 469  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala  
1 5 10 15  
  
Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu  
20 25 30  
  
Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu  
35 40 45  
  
Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His  
50 55 60  
  
Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val  
65 70 75 80  
  
Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu  
85 90 95  
  
Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp  
100 105 110  
  
Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp  
115 120 125  
  
Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu  
130 135 140  
  
Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met  
145 150 155 160  
  
Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met  
165 170 175  
  
Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg  
180 185 190  
  
Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp  
195 200 205  
  
Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu  
210 215 220  
  
Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys  
225 230 235 240  
  
Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu  
245 250 255  
  
Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val  
260 265 270  
  
Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu  
275 280 285  
  
Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly  
290 295 300  
  
Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg  
305 310 315 320  
  
Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe

325

330

335

Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile  
 340 345 350

Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val  
 355 360 365

Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu  
 370 375 380

Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu  
 385 390 395 400

Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg  
 405 410 415

Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln  
 420 425 430

Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr  
 435 440 445

Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro  
 450 455 460

Ser Ser Ser Ala Tyr  
 465

<210> 49

<211> 359

<212> PRT

<213> Cavia porcellus

<400> 49

Met Ile Leu Asn Ser Ser Thr Gln Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15

Asp Cys Pro Lys Asp Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro  
 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60

Val Phe Leu Leu Asn Leu Ala Asp Ile Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95

Gly Asn Tyr Met Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
 100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140

Ala Lys Val Thr Cys Val Ile Ile Trp Leu Met Ala Gly Leu Ala Ser  
 145 150 155 160  
 Leu Pro Ala Val Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175  
 Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190  
 Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Met Phe Pro Phe  
 195 200 205  
 Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220  
 Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
 225 230 235 240  
 Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Val Pro His  
 245 250 255  
 Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile His  
 260 265 270  
 Asp Cys Lys Ile Ser Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285  
 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300  
 Leu Gly Lys Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320  
 Pro Pro Lys Ala Lys Ser His Ser Thr Leu Ser Thr Lys Met Ser Thr  
 325 330 335  
 Leu Ser Tyr Arg Pro Ser Asn Asn Val Ser Ser Ser Ala Lys Lys Pro  
 340 345 350  
 Val Gln Cys Phe Glu Val Glu  
 355

<210> 50  
 <211> 359  
 <212> PRT  
 <213> Cavia porcellus

<400> 50  
 Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15  
 Asp Cys Pro Lys Ala Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro  
 20 25 30  
 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45  
 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60  
 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Ile Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95  
 Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
 100 105 110  
 Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125  
 Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140  
 Ala Lys Val Thr Cys Val Ile Ile Trp Leu Met Ala Gly Leu Ala Ser  
 145 150 155 160  
 Leu Pro Ala Val Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175  
 Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190  
 Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Met Phe Pro Phe  
 195 200 205  
 Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220  
 Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
 225 230 235 240  
 Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Val Pro His  
 245 250 255  
 Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile His  
 260 265 270  
 Asp Cys Lys Ile Ser Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285  
 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300  
 Leu Gly Lys Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320  
 Pro Pro Lys Ala Lys Ser His Ser Thr Leu Ser Thr Lys Met Ser Thr  
 325 330 335  
 Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Ala Lys Lys Pro  
 340 345 350  
 Val Gln Cys Phe Glu Val Glu  
 355

<210> 51  
<211> 359  
<212> PRT  
<213> *Mus musculus*

<400> 51  
Met Ala Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
42

1

5

10

15

Asp Cys Pro Arg Ala Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro  
 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95

Gly Asn His Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
 100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140

Ala Lys Val Thr Cys Ile Ile Trp Leu Met Ala Gly Leu Ala Ser  
 145 150 155 160

Leu Pro Ala Val Ile His Arg Asn Val Tyr Phe Ile Glu Asn Thr Asn  
 165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Arg Asn Ser Thr Leu Pro  
 180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
 195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Arg  
 225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Val Pro His  
 245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Val Ile His  
 260 265 270

Asp Cys Lys Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300

Leu Gly Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Ser Leu Ser Thr Lys Met Ser Thr  
 325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Met Ser Ser Ala Ala Lys Lys Pro

340

345

350

Ala Ser Cys Ser Glu Val Glu  
355

<210> 52  
<211> 359  
<212> PRT  
<213> Mus musculus

<400> 52  
Met Ala Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
1 5 10 15

Asp Cys Pro Arg Ala Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro  
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn His Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Met Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Val Ile His Arg Asn Val Tyr Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Arg Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Arg  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Val Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Val Ile His  
260 265 270

Asp Cys Lys Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile			
275	280	285	
Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe			
290	295	300	
Leu Gly Lys Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile			
305	310	315	320
Pro Pro Lys Ala Lys Ser His Ser Ser Leu Ser Thr Lys Met Ser Thr			
325	330	335	
Leu Ser Tyr Arg Pro Ser Asp Asn Met Ser Ser Ala Ala Lys Lys Pro			
340	345	350	
Ala Ser Cys Ser Glu Val Glu			
355			

<210> 53  
<211> 318  
<212> PRT  
<213> Mus musculus

<220>  
<221> VARIANT  
<222> (286)  
<223> Wherein Xaa is any amino acid.

<400> 53			
Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu			
1	5	10	15

Leu Gly Ile Pro Gly Leu Glu Glu Leu Gln Phe Trp Leu Gly Leu Pro			
20	25	30	

Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu			
35	40	45	

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu			
50	55	60	

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val			
65	70	75	80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe			
85	90	95	

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile			
100	105	110	

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile			
115	120	125	

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys			
130	135	140	

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro			
145	150	155	160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile			
165	170	175	

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val  
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile  
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His  
210 215 220

Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn  
225 230 235 240

Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala  
245 250 255

Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr  
260 265 270

Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu  
275 280 285

Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala  
290 295 300

Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp  
305 310 315

<210> 54

<211> 339

<212> PRT

<213> Mus musculus

<400> 54

Met Pro Glu Lys Met Leu Ser Lys Leu Ile Ala Tyr Leu Leu Ile  
1 5 10 15

Glu Ser Cys Arg Gln Thr Ala Gln Leu Val Lys Gly Arg Arg Ile Trp  
20 25 30

Val Asp Ser Arg Pro His Trp Pro Asn Thr Thr His Tyr Arg Glu Leu  
35 40 45

Glu Asp Gln His Val Trp Ile Ala Ile Pro Phe Cys Ser Met Tyr Ile  
50 55 60

Leu Ala Leu Val Gly Asn Gly Thr Ile Leu Tyr Ile Ile Ile Thr Asp  
65 70 75 80

Arg Ala Leu His Glu Pro Met Tyr Leu Phe Leu Cys Leu Leu Ser Ile  
85 90 95

Thr Asp Leu Val Leu Cys Ser Thr Thr Leu Pro Lys Met Leu Ala Ile  
100 105 110

Phe Trp Leu Arg Ser His Val Ile Ser Tyr His Gly Cys Leu Thr Gln  
115 120 125

Met Phe Phe Val His Ala Val Phe Ala Thr Glu Ser Ala Val Leu Leu  
130 135 140

Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr  
145 150 155 160

Thr Ser Ile Leu Asn Ala Val Val Ile Gly Lys Ile Gly Leu Ala Cys  
165 170 175  
Val Thr Arg Gly Leu Leu Phe Val Phe Pro Phe Val Ile Leu Ile Glu  
180 185 190  
Arg Leu Pro Phe Cys Gly His His Ile Ile Pro His Thr Tyr Cys Glu  
195 200 205  
His Met Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile Lys Pro Asn Thr  
210 215 220  
Ile Tyr Gly Leu Thr Val Ala Leu Ser Val Thr Gly Met Asp Val Val  
225 230 235 240  
Leu Ile Ala Thr Ser Tyr Ile Leu Ile Leu Gln Ala Val Leu Arg Leu  
245 250 255  
Pro Ser Lys Asp Ala Gln Phe Arg Ala Phe Ser Thr Cys Gly Ala His  
260 265 270  
Ile Cys Val Ile Leu Val Phe Tyr Ile Pro Ala Phe Phe Ser Phe Phe  
275 280 285  
Thr His Arg Phe Gly His His Val Pro Pro Gln Val His Ile Ile Leu  
290 295 300  
Ala Asn Leu Tyr Leu Leu Val Pro Pro Val Leu Asn Pro Leu Val Tyr  
305 310 315 320  
Gly Ile Asn Thr Lys Gln Ile Arg Leu Arg Ile Leu Asp Phe Phe Val  
325 330 335  
Lys Arg Arg

<210> 55  
<211> 318  
<212> PRT  
<213> Homo sapiens

<400> 55  
Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe  
1 5 10 15  
Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile  
20 25 30  
Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu  
35 40 45  
Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu  
50 55 60  
Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr  
65 70 75 80  
Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser  
85 90 95  
Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala  
47

100	105	110
Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala		
115	120	125
Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile		
130	135	140
Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser		
145	150	155
160		
Pro Phe Ile Phe Leu Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val		
165	170	175
Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys		
180	185	190
Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu		
195	200	205
Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile		
210	215	220
Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala		
225	230	235
240		
Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile		
245	250	255
Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val		
260	265	270
Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro		
275	280	285
Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg		
290	295	300
Ser Arg Leu Leu Lys Leu Leu His Leu Gly Lys Thr Ser Ile		
305	310	315
<210> 56		
<211> 321		
<212> PRT		
<213> Mus musculus		
<400> 56		
Met Asn Ser Lys Ala Ser Met Leu Gly Thr Asn Phe Thr Ile Ile His		
1	5	10
15		
Pro Thr Val Phe Ile Leu Leu Gly Ile Pro Gly Leu Glu Gln Tyr His		
20	25	30
Thr Trp Leu Ser Ile Pro Phe Cys Leu Met Tyr Ile Ala Ala Val Leu		
35	40	45
Gly Asn Gly Ala Leu Ile Leu Val Val Leu Ser Glu Arg Thr Leu His		
50	55	60
Glu Pro Met Tyr Val Phe Leu Ser Met Leu Ala Gly Thr Asp Ile Leu		
65	70	75
80		

Leu	Ser	Thr	Thr	Thr	Val	Pro	Lys	Thr	Leu	Ala	Ile	Phe	Trp	Phe	His
85								90					95		
Ala	Gly	Glu	Ile	Pro	Phe	Asp	Ala	Cys	Ile	Ala	Gln	Met	Phe	Phe	Ile
100								105					110		
His	Val	Ala	Phe	Val	Ala	Glu	Ser	Gly	Ile	Leu	Leu	Ala	Met	Ala	Phe
115								120					125		
Asp	Arg	Tyr	Val	Ala	Ile	Cys	Thr	Pro	Leu	Arg	Tyr	Ser	Ala	Val	Leu
130								135					140		
Thr	Pro	Met	Ala	Ile	Gly	Lys	Met	Thr	Leu	Ala	Ile	Trp	Gly	Arg	Ser
145								150					155		160
Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ile	Phe	Leu	Leu	Lys	Arg	Leu	Ser	Tyr
165								170					175		
Cys	Arg	Thr	Asn	Val	Ile	Pro	His	Ser	Tyr	Cys	Glu	His	Ile	Gly	Val
180								185					190		
Ala	Arg	Leu	Ala	Cys	Ala	Asp	Ile	Thr	Val	Asn	Ile	Trp	Tyr	Gly	Phe
195								200					205		
Ser	Val	Pro	Met	Ala	Ser	Val	Leu	Val	Asp	Val	Ala	Leu	Ile	Gly	Ile
210								215					220		
Ser	Tyr	Thr	Leu	Ile	Leu	Gln	Ala	Val	Phe	Arg	Leu	Pro	Ser	Gln	Asp
225								230					235		240
Ala	Arg	His	Lys	Ala	Leu	Asn	Thr	Cys	Gly	Ser	His	Ile	Gly	Val	Ile
245								250					255		
Leu	Leu	Phe	Phe	Ile	Pro	Ser	Phe	Phe	Thr	Phe	Leu	Thr	His	Arg	Phe
260								265					270		
Gly	Lys	Asn	Ile	Pro	His	His	Val	His	Ile	Leu	Leu	Ala	Asn	Leu	Tyr
275								280					285		
Val	Leu	Val	Pro	Pro	Met	Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Ala	Lys	Thr
290								295					300		
Lys	Gln	Ile	Arg	Asp	Ser	Met	Thr	Arg	Met	Leu	Ser	Val	Val	Trp	Lys
305														320	
Ser															

<210> 57  
 <211> 326  
 <212> PRT  
 <213> Mus musculus

<400> 57  
 Met Lys Val Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val  
 1 5 10 15  
 Trp Tyr Val Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp  
 20 25 30  
 Ile Ala Ile Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn  
 35 40 45

Val	Leu	Leu	Ile	Phe	Leu	Ile	Val	Thr	Glu	Arg	Ser	Leu	His	Glu	Pro
50						55						60			
Met	Tyr	Phe	Phe	Leu	Ser	Met	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Leu	Ser
65						70					75				80
Thr	Ala	Thr	Ala	Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	His	Ser	Arg
						85					90				95
Gly	Ile	Ser	Phe	Gly	Ser	Cys	Val	Ser	Gln	Met	Phe	Phe	Ile	His	Phe
						100				105				110	
Ile	Phe	Val	Ala	Glu	Ser	Ala	Ile	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg
						115				120				125	
Tyr	Val	Ala	Ile	Cys	Tyr	Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Thr	Ser
						130				135				140	
Ser	Val	Ile	Gly	Lys	Ile	Gly	Thr	Ala	Ala	Val	Val	Arg	Ser	Phe	Leu
						145				150			155		160
Ile	Cys	Phe	Pro	Phe	Ile	Phe	Leu	Val	Tyr	Arg	Leu	Leu	Tyr	Cys	Gly
						165				170				175	
Lys	His	Ile	Ile	Pro	His	Ser	Tyr	Cys	Glu	His	Met	Gly	Ile	Ala	Arg
						180				185				190	
Leu	Ala	Cys	Asp	Asn	Ile	Thr	Val	Asn	Ile	Ile	Tyr	Gly	Leu	Thr	Met
						195				200				205	
Ala	Leu	Leu	Ser	Thr	Gly	Leu	Asp	Ile	Leu	Leu	Ile	Ile	Ile	Ser	Tyr
						210				215				220	
Thr	Met	Ile	Leu	Arg	Thr	Val	Phe	Gln	Ile	Pro	Ser	Trp	Ala	Ala	Arg
						225				230				240	
Tyr	Lys	Ala	Leu	Asn	Thr	Cys	Gly	Ser	His	Ile	Cys	Val	Ile	Leu	Leu
						245				250				255	
Phe	Tyr	Thr	Pro	Ala	Phe	Phe	Ser	Phe	Phe	Ala	His	Arg	Phe	Gly	Gly
						260				265				270	
Lys	Thr	Val	Pro	Arg	His	Ile	His	Ile	Leu	Val	Ala	Asn	Leu	Tyr	Val
						275				280				285	
Val	Val	Pro	Pro	Met	Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Val	Lys	Thr	Lys
						290				295				300	
Gln	Ile	Gln	Asp	Arg	Val	Val	Phe	Leu	Phe	Ser	Ser	Val	Ser	Thr	Cys
						305				310				315	
Gln	His	Asp	Ser	Arg	Cys										320

<210> 58

<211> 319

<212> PRT

<213> Mus musculus

<400> 58

Met Ala Thr Ser Asn Ser Ser Thr Ile Val Ser Ser Thr Phe Tyr Leu

1

5

10

15

Thr Gly Ile Pro Gly Tyr Glu Glu Phe His His Trp Ile Ser Ile Pro  
20 25 30

Phe Cys Phe Leu Tyr Leu Val Gly Ile Thr Gly Asn Cys Met Ile Leu  
35 40 45

His Ile Val Arg Thr Asp Pro Arg Leu His Glu Pro Met Tyr Tyr Phe  
50 55 60

Leu Ala Met Leu Ser Leu Thr Asp Met Ala Met Ser Leu Pro Thr Met  
65 70 75 80

Met Ser Leu Phe Arg Val Leu Trp Ser Ile Ser Arg Glu Ile Gln Phe  
85 90 95

Asn Ile Cys Val Val Gln Met Phe Leu Ile His Thr Phe Ser Phe Thr  
100 105 110

Glu Ser Ser Val Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile  
115 120 125

Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Pro Lys Leu Ile Ala  
130 135 140

Lys Ile Gly Thr Ala Ala Leu Leu Arg Ser Ser Ile Leu Ile Ile Pro  
145 150 155 160

Leu Ile Ala Arg Leu Ala Phe Phe Pro Phe Cys Gly Ser His Val Leu  
165 170 175

Ser His Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Ala Cys Ala  
180 185 190

Asp Ile Arg Phe Asn Val Ile Tyr Gly Leu Val Leu Ile Thr Leu Leu  
195 200 205

Trp Gly Met Asp Ser Leu Gly Ile Phe Val Ser Tyr Val Leu Ile Leu  
210 215 220

His Ser Val Leu Lys Ile Ala Ser Arg Glu Gly Arg Leu Lys Ala Leu  
225 230 235 240

Asn Thr Cys Ala Ser His Ile Cys Ala Val Leu Ile Leu Tyr Val Pro  
245 250 255

Met Ile Gly Leu Ser Ile Val His Arg Phe Ala Lys His Ser Ser Pro  
260 265 270

Leu Ile His Ile Phe Met Ala His Ile Tyr Leu Leu Val Pro Pro Val  
275 280 285

Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Glu Gly  
290 295 300

Ile Leu His Leu Leu Cys Ser Pro Lys Ile Ser Ser Ile Thr Met  
305 310 315

<210> 59

<211> 317

<212> PRT

<213> Mus musculus

<400> 59

Met	Lys	Val	Ser	Ile	Pro	Pro	Arg	Ala	Asn	Phe	Ser	Tyr	Ala	Ile	Phe
1				5				10					15		
Leu	Leu	Thr	Gly	Phe	Pro	Gly	Leu	Glu	Trp	Ala	His	His	Trp	Ile	Ser
		20					25				30				
Leu	Pro	Ile	Phe	Met	Gly	Tyr	Phe	Val	Ala	Ile	Met	Gly	Asn	Ala	Thr
	35					40				45					
Ile	Leu	His	Leu	Val	Arg	Thr	Asp	Pro	Ser	Leu	His	Gln	Pro	Met	Tyr
	50				55				60						
Tyr	Phe	Leu	Ala	Ile	Leu	Ala	Val	Thr	Asp	Leu	Gly	Leu	Cys	Met	Ser
	65				70			75			80				
Thr	Leu	Pro	Ser	Val	Leu	Gly	Val	Leu	Trp	Phe	Asp	Ala	Arg	Met	Val
		85					90				95				
Gly	Leu	Val	Pro	Cys	Val	Leu	Gln	Gln	His	Phe	Leu	His	Ser	Phe	Ser
		100				105			110						
Phe	Met	Glu	Ser	Ala	Val	Leu	Phe	Ala	Met	Ala	Leu	Asp	Arg	Leu	Ile
	115				120				125						
Ala	Ile	Arg	Phe	Pro	Leu	Arg	Tyr	Ala	Ser	Val	Leu	Thr	Gly	Pro	Arg
	130				135			140							
Val	Ala	Leu	Ile	Gly	Thr	Val	Leu	Gly	Met	Arg	Ser	Ala	Ala	Ile	Thr
	145			150			155			160					
Ala	Ala	Pro	Ser	Leu	His	Leu	Leu	Thr	Phe	Asp	Tyr	Cys	His	Pro	Gly
		165				170		175							
Ala	Leu	Ser	His	Ala	Tyr	Cys	Leu	His	Gln	Asp	Met	Ile	Arg	Leu	Ala
		180				185		190							
Cys	Ser	Asp	Thr	Arg	Phe	Asn	Arg	Leu	Tyr	Gly	Leu	Cys	Ile	Ile	Met
	195				200			205							
Leu	Ala	Met	Gly	Ser	Asp	Val	Leu	Phe	Ile	Leu	Leu	Ser	Tyr	Ala	Val
	210				215			220							
Ile	Leu	Arg	Thr	Val	Leu	Ala	Ile	Ala	Ser	Ala	Gly	Glu	Arg	Leu	Lys
	225				230			235			240				
Ala	Leu	Asn	Thr	Cys	Val	Ser	His	Ile	Leu	Ala	Val	Leu	Cys	Phe	Tyr
		245				250		255							
Val	Pro	Val	Leu	Gly	Leu	Ser	Ile	Val	His	Arg	Phe	Gly	Gln	His	Thr
	260				265			270							
Ser	Pro	Leu	Val	His	Ile	Leu	Met	Gly	Thr	Val	Ser	Val	Leu	Phe	Pro
	275					280		285							
Pro	Val	Met	Asn	Pro	Val	Ile	Tyr	Ser	Ile	Lys	Thr	Gln	Gln	Ile	Arg
	290				295			300							
Arg	Ala	Ile	Val	Lys	Val	Ile	Ser	Leu	Gly	Lys	Ile	Gln			
	305				310			315							

<210> 60  
<211> 314  
<212> PRT  
<213> Homo sapiens

<400> 60  
Met Leu Gly Leu Asn Gly Thr Pro Phe Gln Pro Ala Thr Leu Gln Leu  
1 5 10 15  
Thr Gly Ile Pro Gly Ile Gln Thr Gly Leu Thr Trp Val Ala Leu Ile  
20 25 30  
Phe Cys Ile Leu Tyr Met Ile Ser Ile Val Gly Asn Leu Ser Ile Leu  
35 40 45  
Thr Leu Val Phe Trp Glu Pro Ala Leu His Gln Pro Met Tyr Tyr Phe  
50 55 60  
Leu Ser Met Leu Ala Leu Asn Asp Leu Gly Val Ser Phe Ser Thr Leu  
65 70 75 80  
Pro Thr Val Ile Ser Thr Phe Cys Phe Asn Tyr Asn His Val Ala Phe  
85 90 95  
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Ser Phe Met  
100 105 110  
Glu Ser Gly Ile Leu Leu Ala Met Ser Leu Asp Arg Phe Val Ala Ile  
115 120 125  
Cys Tyr Pro Leu Arg Tyr Val Thr Val Leu Thr His Asn Arg Ile Leu  
130 135 140  
Ala Met Gly Leu Gly Ile Leu Thr Lys Ser Phe Thr Thr Leu Phe Pro  
145 150 155 160  
Phe Pro Phe Val Val Lys Arg Leu Pro Phe Cys Lys Gly Asn Val Leu  
165 170 175  
His His Ser Tyr Cys Leu His Pro Asp Leu Met Lys Val Ala Cys Gly  
180 185 190  
Asp Ile His Val Asn Asn Ile Tyr Gly Leu Leu Val Ile Ile Phe Thr  
195 200 205  
Tyr Gly Met Asp Ser Thr Phe Ile Leu Leu Ser Tyr Ala Leu Ile Leu  
210 215 220  
Arg Ala Met Leu Val Ile Ile Ser Gln Glu Gln Arg Leu Lys Ala Leu  
225 230 235 240  
Asn Thr Cys Met Ser His Ile Cys Ala Val Leu Ala Phe Tyr Val Pro  
245 250 255  
Ile Ile Ala Val Ser Met Ile His Arg Phe Trp Lys Ser Ala Pro Pro  
260 265 270  
Val Val His Val Met Met Ser Asn Val Tyr Leu Phe Val Pro Pro Met  
275 280 285  
Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Glu Ile Arg Lys Gly  
290 295 300

Ile Leu Lys Phe Phe His Lys Ser Gln Ala  
305 310

<210> 61  
<211> 312  
<212> PRT  
<213> Homo sapiens

<400> 61  
Met Gly Leu Phe Asn Val Thr His Pro Ala Phe Phe Leu Leu Thr Gly  
1 5 10 15

Ile Pro Gly Leu Glu Ser Ser His Ser Trp Leu Ser Gly Pro Leu Cys  
20 25 30

Val Met Tyr Ala Val Ala Leu Gly Gly Asn Thr Val Ile Leu Gln Ala  
35 40 45

Val Arg Val Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser  
50 55 60

Met Leu Ser Phe Ser Asp Val Ala Ile Ser Met Ala Thr Leu Pro Thr  
65 70 75 80

Val Leu Arg Thr Phe Cys Leu Asn Ala Arg Asn Ile Thr Phe Asp Ala  
85 90 95

Cys Leu Ile Gln Met Phe Leu Ile His Phe Phe Ser Met Met Glu Ser  
100 105 110

Gly Ile Leu Leu Ala Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Asp  
115 120 125

Pro Leu Arg Tyr Ala Thr Val Leu Thr Thr Glu Val Ile Ala Ala Met  
130 135 140

Gly Leu Gly Ala Ala Ala Arg Ser Phe Ile Thr Leu Phe Pro Leu Pro  
145 150 155 160

Phe Leu Ile Lys Arg Leu Pro Ile Cys Arg Ser Asn Val Leu Ser His  
165 170 175

Ser Tyr Cys Leu His Pro Asp Met Met Arg Leu Ala Cys Ala Asp Ile  
180 185 190

Ser Ile Asn Ser Ile Tyr Gly Leu Phe Val Leu Val Ser Thr Phe Gly  
195 200 205

Met Asp Leu Phe Phe Ile Phe Leu Ser Tyr Val Leu Ile Leu Arg Ser  
210 215 220

Val Met Ala Thr Ala Ser Arg Glu Glu Arg Leu Lys Ala Leu Asn Thr  
225 230 235 240

Cys Val Ser His Ile Leu Ala Val Leu Ala Phe Tyr Val Pro Met Ile  
245 250 255

Gly Val Ser Thr Val His Arg Phe Gly Lys His Val Pro Cys Tyr Ile  
260 265 270

His Val Leu Met Ser Asn Val Tyr Leu Phe Val Pro Pro Val Leu Asn

275

280

285

Pro Leu Ile Tyr Ser Ala Lys Thr Lys Glu Ile Arg Arg Ala Ile Phe  
 290 295 300

Arg Met Phe His His Ile Lys Ile  
 305 310

<210> 62  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Met Ser Ser Ser Ser Ser His Pro Phe Leu Leu Thr Gly Phe Pro  
 1 5 10 15

Gly Leu Glu Glu Ala His His Trp Ile Ser Val Phe Phe Leu Phe Met  
 20 25 30

Tyr Ile Ser Ile Leu Phe Gly Asn Gly Thr Leu Leu Leu Leu Ile Lys  
 35 40 45

Glu Asp His Asn Leu His Glu Pro Met Tyr Phe Phe Leu Ala Met Leu  
 50 55 60

Ala Ala Thr Asp Leu Gly Leu Ala Leu Thr Thr Met Pro Thr Val Leu  
 65 70 75 80

Gly Val Leu Trp Leu Asp His Arg Glu Ile Gly Ser Ala Ala Cys Phe  
 85 90 95

Ser Gln Ala Tyr Phe Ile His Ser Leu Ser Phe Leu Glu Ser Gly Ile  
 100 105 110

Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu  
 115 120 125

Arg Tyr Thr Ser Val Leu Thr Asn Thr Arg Val Val Lys Ile Gly Leu  
 130 135 140

Gly Val Leu Met Arg Gly Phe Val Ser Val Val Pro Pro Ile Arg Pro  
 145 150 155 160

Leu Tyr Phe Phe Leu Tyr Cys His Ser His Val Leu Ser His Ala Phe  
 165 170 175

Cys Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Thr Thr Phe  
 180 185 190

Asn Arg Leu Tyr Pro Ala Val Leu Val Val Phe Ile Phe Val Leu Asp  
 195 200 205

Tyr Leu Ile Ile Phe Ile Ser Tyr Val Leu Ile Leu Lys Thr Val Leu  
 210 215 220

Ser Ile Ala Ser Arg Glu Glu Arg Ala Lys Ala Leu Ile Thr Cys Val  
 225 230 235 240

Ser His Ile Cys Cys Val Leu Val Phe Tyr Val Thr Val Ile Gly Leu  
 245 250 255

Ser Leu Ile His Arg Phe Gly Lys Gln Val Pro His Ile Val His Leu  
260 265 270

Ile Met Ser Tyr Ala Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Ile  
275 280 285

Thr Tyr Ser Val Lys Thr Lys Gln Ile Gln Asn Ala Ile Leu His Leu  
290 295 300

Phe Thr Thr His Arg Ile Gly Thr  
305 310

<210> 63  
<211> 318  
<212> PRT  
<213> Mus musculus

<220>  
<221> VARIANT  
<222> (286)  
<223> Wherein Xaa is any amino acid.

<400> 63  
Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu  
1 5 10 15

Leu Gly Ile Pro Gly Leu Glu Leu Gln Phe Trp Leu Gly Leu Pro  
20 25 30

Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu  
35 40 45

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu  
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val  
65 70 75 80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe  
85 90 95

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile  
100 105 110

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile  
115 120 125

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys  
130 135 140

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro  
145 150 155 160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile  
165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val  
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile  
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His  
 210 215 220  
 Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala  
 245 250 255  
 Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr  
 260 265 270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala  
 290 295 300  
 Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp  
 305 310 315  
  
 <210> 64  
 <211> 320  
 <212> PRT  
 <213> Rattus norvegicus  
  
 <400> 64  
 Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile  
 1 5 10 15  
 Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser  
 20 25 30  
 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val  
 35 40 45  
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
 50 55 60  
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
 65 70 75 80  
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys  
 85 90 95  
 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
 100 105 110  
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
 115 120 125  
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly  
 130 135 140  
 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu  
 145 150 155 160  
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser  
 165 170 175  
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu  
 180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val  
195 200 205  
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val  
210 215 220  
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys  
225 230 235 240  
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly  
245 250 255  
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His  
260 265 270  
Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro  
275 280 285  
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala  
290 295 300  
Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr  
305 310 315 320

<210> 65  
<211> 320  
<212> PRT  
<213> Homo sapiens

<400> 65  
Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile  
1 5 10 15

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
20 25 30

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
35 40 45

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
50 55 60

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
65 70 75 80

Leu Ala Ala Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys  
85 90 95

Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
100 105 110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly  
130 135 140

Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu  
58

145	150	155	160
Leu Ile Lys Arg	Leu Ala Phe Cys His	Ser Asn Val	Leu Ser His Ser
165	170		175
Tyr Cys Val His Gln Asp	Val Met Lys	Leu Ala Tyr Ala Asp	Thr Leu
180	185	190	
Pro Asn Val Val Tyr Gly	Leu Thr Ala Ile	Leu Leu Val Met Gly Val	
195	200	205	
Asp Val Met Phe Ile Ser	Leu Ser Tyr Phe	Leu Ile Ile Arg Thr Val	
210	215	220	
Leu Gln Leu Pro Ser Lys	Ser Glu Arg Ala	Lys Ala Phe Gly Thr Cys	
225	230	235	240
Val Ser His Ile Gly Val Val	Leu Ala Phe Tyr Val Pro	Leu Ile Gly	
245	250	255	
Leu Ser Val Val His Arg Phe Gly	Asn Ser Leu His Pro	Ile Val Arg	
260	265	270	
Val Val Met Gly Asp Ile Tyr	Leu Leu Pro Pro Val	Ile Asn Pro	
275	280	285	
Ile Ile Tyr Gly Ala Lys Thr	Lys Gln Ile Arg Thr Arg	Val Leu Ala	
290	295	300	
Met Phe Lys Ile Ser Cys Asp	Lys Asp Leu Gln Ala Val	Gly Gly Lys	
305	310	315	320

<210> 66  
 <211> 316  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Met Pro Thr Phe Asn Gly Ser Val Phe Met Pro Ser Ala Phe Ile Leu  
 1 5 10 15

Ile Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro  
 20 25 30

Phe Ser Ala Met Tyr Leu Ile Gly Val Ile Gly Asn Ser Leu Ile Leu  
 35 40 45

Val Ile Ile Lys Tyr Glu Asn Ser Leu His Ile Pro Met Tyr Ile Phe  
 50 55 60

Leu Ala Met Leu Ala Ala Thr Asp Ile Ala Leu Asn Thr Cys Ile Leu  
 65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe His Leu Pro Glu Ile Ser Phe  
 85 90 95

Asp Ala Cys Leu Phe Gln Met Trp Leu Ile His Ser Phe Gln Ala Ile  
 100 105 110

Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile  
115 120 125

Cys Ile Pro Leu Arg His Ala Thr Ile Phe Ser Gln Gln Phe Leu Thr  
130 135 140

His Ile Gly Leu Gly Val Thr Leu Arg Ala Ala Ile Leu Ile Ile Pro  
145 150 155 160

Ser Leu Gly Leu Ile Lys Cys Cys Leu Lys His Tyr Arg Thr Thr Val  
165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Thr  
180 185 190

Glu Asp Ile Arg Val Asn Lys Ile Tyr Gly Leu Phe Val Ala Phe Ala  
195 200 205

Ile Leu Gly Phe Asp Ile Ile Phe Ile Thr Leu Ser Tyr Val Gln Ile  
210 215 220

Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala  
225 230 235 240

Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu  
245 250 255

Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ser His Ile Pro  
260 265 270

Pro Tyr Ile His Ile Leu Leu Ser Asn Leu Tyr Leu Leu Val Pro Pro  
275 280 285

Phe Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp  
290 295 300

His Ile Val Lys Val Phe Phe Lys Lys Val Thr  
305 310 315

<210> 67  
<211> 316  
<212> PRT  
<213> Mus musculus

<400> 67  
Met Pro His Leu Asn Ser Thr Ile Phe Arg Pro Ser Val Leu Thr Leu  
1 5 10 15

Thr Gly Ile Pro Gly Leu Glu Ser Val Gln Phe Trp Ile Gly Ile Pro  
20 25 30

Phe Cys Ile Met Tyr Ile Ile Ala Leu Leu Gly Asn Ser Leu Leu Leu  
35 40 45

Val Val Ile Lys Val Glu Arg Ser Leu His Glu Pro Met Tyr Leu Phe  
50 55 60

Leu Ala Met Leu Gly Ala Thr Asp Ile Ser Leu Ser Thr Ser Ile Leu  
65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe His Leu Ser Thr Ile Tyr Phe  
85 90 95  
60

Asp Ala Cys Leu Leu Gln Met Trp Leu Ile His Thr Phe Gln Gly Ile  
100 105 110

Glu Ser Gly Ile Leu Phe Ala Met Ala Met Asp Arg Tyr Val Ala Ile  
115 120 125

Cys Asp Pro Leu Arg His Ala Ser Ile Phe Thr Gln Arg Leu Leu Thr  
130 135 140

Gln Ile Gly Val Gly Val Thr Leu Arg Ala Ala Leu Phe Val Ala Pro  
145 150 155 160

Cys Leu Phe Leu Ile Lys Cys Arg Leu Lys Phe Tyr Trp Thr Thr Val  
165 170 175

Val Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala  
180 185 190

Glu Asp Val His Val Asn Lys Ile Tyr Gly Leu Phe Val Ala Phe Ser  
195 200 205

Ile Leu Gly Leu Asp Ile Ile Phe Ile Thr Leu Ser Tyr Ile Arg Ile  
210 215 220

Phe Ile Thr Val Phe Lys Leu Pro Gln Lys Glu Ala Arg Leu Lys Ala  
225 230 235 240

Phe Asn Thr Cys Val Ala His Ile Cys Val Phe Leu Glu Phe Tyr Leu  
245 250 255

Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Tyr His Val Pro  
260 265 270

Ser Tyr Ile His Ile Leu Leu Ser Asn Leu Tyr Leu Leu Val Pro Pro  
275 280 285

Leu Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp  
290 295 300

Gln Val Ser Lys Ile Leu Tyr Cys Asn Tyr Ser Tyr  
305 310 315

<210> 68  
<211> 315  
<212> PRT  
<213> Mus musculus

<400> 68

Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro Ser Val Leu Thr Leu  
1 5 10 15

Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro  
20 25 30

Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu  
35 40 45

Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe  
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu  
61

65	70	75	80
Pro Lys Met Leu Gly Ile Phe Trp Phe His Met Pro Gln Ile Ser Phe			
85	90		95
Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His Ser Phe Gln Ala Thr			
100	105		110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile			
115	120		125
Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser Pro Gln Leu Thr Thr			
130	135	140	
Cys Leu Gly Ala Gly Ala Leu Leu Arg Ala Phe Ile Leu Val Ser Pro			
145	150	155	160
Ser Ile Leu Leu Ile Lys Cys Arg Leu Lys Tyr Phe Arg Thr Thr Ile			
165	170		175
Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala			
180	185		190
Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu Leu Val Ala Phe Ala			
195	200		205
Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe Ser Tyr Val Arg Ile			
210	215		220
Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala			
225	230	235	240
Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu			
245	250		255
Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ala His Ile Pro			
260	265		270
Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr Leu Leu Val Pro Pro			
275	280	285	
Phe Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp			
290	295	300	
Gln Val Leu Lys Met Leu Phe Ser Lys Lys His			
305	310	315	
<210> 69			
<211> 316			
<212> PRT			
<213> Mus musculus			
<400> 69			
Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro Ser Val Leu Thr Leu			
1	5	10	15
Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro			
20	25	30	
Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu			
35	40	45	

Val	Ile	Ile	Lys	Ser	Glu	Lys	Ser	Leu	His	Ile	Pro	Met	Tyr	Ile	Phe
50					55					60					
Leu	Ala	Ile	Leu	Ala	Val	Thr	Asp	Ile	Ala	Leu	Ser	Thr	Cys	Ile	Leu
65					70					75			80		
Pro	Lys	Met	Leu	Gly	Ile	Phe	Trp	Phe	His	Met	Pro	Gln	Ile	Ser	Phe
					85				90			95			
Asp	Ala	Cys	Leu	Leu	Gln	Met	Glu	Leu	Ile	His	Ser	Phe	Gln	Ala	Thr
					100				105			110			
Glu	Ser	Gly	Ile	Leu	Leu	Ala	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile
					115				120			125			
Cys	Asn	Pro	Leu	Arg	His	Ala	Thr	Ile	Phe	Ser	Pro	Gln	Leu	Thr	Thr
					130				135			140			
Cys	Leu	Gly	Ala	Gly	Ala	Leu	Leu	Arg	Ser	Leu	Ile	Thr	Thr	Phe	Pro
					145				150			155			160
Leu	Ile	Leu	Leu	Ile	Lys	Phe	Cys	Leu	Lys	Tyr	Phe	Arg	Thr	Thr	Ile
					165				170			175			
Ile	Ser	His	Ser	Tyr	Cys	Glu	His	Met	Ala	Ile	Val	Lys	Leu	Ala	Ala
					180				185			190			
Gln	Asp	Ile	Arg	Ile	Asn	Lys	Ile	Cys	Gly	Leu	Leu	Val	Ala	Phe	Ala
					195				200			205			
Ile	Leu	Gly	Phe	Asp	Ile	Val	Phe	Ile	Thr	Phe	Ser	Tyr	Val	Arg	Ile
					210				215			220			
Phe	Ile	Thr	Val	Phe	Gln	Leu	Pro	Gln	Lys	Glu	Ala	Arg	Phe	Lys	Ala
					225				230			235			240
Phe	Asn	Thr	Cys	Ile	Ala	His	Ile	Cys	Val	Phe	Leu	Gln	Phe	Tyr	Leu
					245				250			255			
Leu	Ala	Phe	Phe	Ser	Phe	Phe	Thr	His	Arg	Phe	Gly	Ala	His	Ile	Pro
					260				265			270			
Pro	Tyr	Val	His	Ile	Leu	Leu	Ser	Asp	Leu	Tyr	Leu	Leu	Val	Pro	Pro
					275				280			285			
Phe	Leu	Asn	Pro	Ile	Val	Tyr	Gly	Ile	Lys	Thr	Lys	Gln	Ile	Arg	Asp
					290				295			300			
Gln	Val	Leu	Lys	Met	Phe	Phe	Ser	Lys	Lys	Pro	Leu				
					305				310			315			

<210> 70  
 <211> 319  
 <212> PRT  
 <213> Gallus gallus

<400> 70  
 Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu Ala Gly  
 1 5 10 15  
 Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro Phe Gly  
 20 25 30

Leu	Met	Tyr	Leu	Val	Ala	Val	Leu	Gly	Asn	Gly	Thr	Ile	Leu	Leu	Val
35							40					45			
Val	Arg	Val	His	Arg	Gln	Leu	His	Gln	Pro	Met	Tyr	Tyr	Phe	Leu	Leu
50						55					60				
Met	Leu	Ala	Thr	Thr	Asp	Leu	Gly	Leu	Thr	Leu	Ser	Thr	Leu	Pro	Thr
65						70			75				80		
Val	Leu	Arg	Val	Phe	Trp	Leu	Gly	Ala	Met	Glu	Ile	Ser	Phe	Pro	Ala
85							90				95				
Cys	Leu	Ile	Gln	Met	Phe	Cys	Ile	His	Val	Phe	Ser	Phe	Met	Glu	Ser
100							105				110				
Ser	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Cys
115							120				125				
Pro	Leu	Arg	Tyr	Ser	Ser	Ile	Leu	Thr	Gly	Ala	Arg	Val	Ala	Gln	Ile
130						135			140						
Gly	Leu	Gly	Ile	Ile	Cys	Arg	Cys	Thr	Leu	Ser	Leu	Leu	Pro	Leu	Ile
145						150			155				160		
Cys	Leu	Leu	Thr	Trp	Leu	Pro	Phe	Cys	Arg	Ser	His	Val	Leu	Ser	His
						165			170			175			
Pro	Tyr	Cys	Leu	His	Gln	Asp	Ile	Ile	Arg	Leu	Ala	Cys	Thr	Asp	Ala
						180			185			190			
Thr	Leu	Asn	Ser	Leu	Tyr	Gly	Leu	Ile	Leu	Val	Leu	Val	Ala	Ile	Leu
						195			200			205			
Asp	Phe	Val	Leu	Ile	Ala	Leu	Ser	Tyr	Ile	Met	Ile	Phe	Arg	Thr	Val
						210			215			220			
Leu	Gly	Ile	Thr	Ser	Lys	Glu	Glu	Gln	Thr	Lys	Ala	Leu	Asn	Thr	Cys
						225			230			235			240
Val	Ser	His	Phe	Cys	Ala	Val	Leu	Ile	Phe	Tyr	Ile	Pro	Leu	Ala	Gly
						245			250			255			
Leu	Ser	Ile	Ile	His	Arg	Tyr	Gly	Arg	Asn	Ala	Pro	Pro	Ile	Ser	His
						260			265			270			
Ala	Val	Met	Ala	Asn	Val	Tyr	Leu	Phe	Val	Pro	Pro	Ile	Leu	Asn	Pro
						275			280			285			
Val	Leu	Tyr	Ser	Met	Lys	Ser	Lys	Ala	Ile	Cys	Lys	Gly	Leu	Leu	Arg
						290			295			300			
Leu	Leu	Cys	Gln	Arg	Ala	Ala	Trp	Pro	Gly	His	Ala	Gln	Asn	Cys	
						305			310			315			

<210> 71  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:pfam00001

7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 71  
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
1 5 10 15  
Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30  
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
35 40 45  
Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
50 55 60  
Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
65 70 75 80  
Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
85 90 95  
Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
100 105 110  
Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
115 120 125  
Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
130 135 140  
Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
145 150 155 160  
Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
165 170 175  
Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
180 185 190  
Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val  
195 200 205  
Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
210 215 220  
Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
225 230 235 240  
Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
245 250

<210> 72

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00001  
7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 72

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg

1	5	10	15
Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu			
20	25	30	
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly			
35	40	45	
Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe			
50	55	60	
Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile			
65	70	75	80
Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg			
85	90	95	
Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala			
100	105	110	
Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val			
115	120	125	
Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser			
130	135	140	
Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu			
145	150	155	160
Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu			
165	170	175	
Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser			
180	185	190	
Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val			
195	200	205	
Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys			
210	215	220	
Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu			
225	230	235	240
Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr			
245	250		

<210> 73  
<211> 254  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:pfam00001  
7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 73  
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
1 5 10 15  
  
Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30

Phe	Leu	Leu	Thr	Leu	Pro	Pro	Trp	Ala	Leu	Tyr	Tyr	Leu	Val	Gly	Gly
35															45
Asp	Trp	Val	Phe	Gly	Asp	Ala	Leu	Cys	Lys	Leu	Val	Gly	Ala	Leu	Phe
50															60
Val	Val	Asn	Gly	Tyr	Ala	Ser	Ile	Leu	Leu	Leu	Thr	Ala	Ile	Ser	Ile
65															80
Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	Leu	Arg	Tyr	Arg	Arg	Ile	Arg
	85									90					95
Thr	Pro	Arg	Arg	Ala	Lys	Val	Leu	Ile	Leu	Leu	Val	Trp	Val	Leu	Ala
	100								105						110
Leu	Leu	Leu	Ser	Leu	Pro	Pro	Leu	Leu	Phe	Ser	Trp	Leu	Arg	Thr	Val
	115								120						125
Glu	Glu	Gly	Asn	Thr	Thr	Val	Cys	Leu	Ile	Asp	Phe	Pro	Glu	Glu	Ser
	130						135						140		
Val	Lys	Arg	Ser	Tyr	Val	Leu	Leu	Ser	Thr	Leu	Val	Gly	Phe	Leu	Leu
	145						150				155				160
Pro	Leu	Leu	Val	Ile	Leu	Val	Cys	Tyr	Thr	Arg	Ile	Leu	Arg	Thr	Leu
				165					170						175
Arg	Lys	Ser	Ala	Arg	Ser	Gln	Arg	Ser	Leu	Lys	Arg	Arg	Ser	Ser	Ser
									180						190
Glu	Arg	Lys	Ala	Ala	Lys	Met	Leu	Leu	Val	Val	Val	Val	Val	Phe	Val
							195			200					205
Leu	Cys	Trp	Leu	Pro	Tyr	His	Ile	Val	Leu	Leu	Leu	Asp	Ser	Leu	Cys
	210						215								220
Leu	Leu	Ser	Ile	Trp	Arg	Val	Leu	Pro	Thr	Ala	Leu	Leu	Ile	Thr	Leu
	225									230					240
Trp	Leu	Ala	Tyr	Val	Asn	Ser	Cys	Leu	Asn	Pro	Ile	Ile	Tyr		
				245											250

<210> 74  
<211> 254  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:pfam00001  
7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 74  
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
1 5 10 15  
Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30  
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
35 40 45

Asp	Trp	Val	Phe	Gly	Asp	Ala	Leu	Cys	Lys	Leu	Val	Gly	Ala	Leu	Phe
50					55					60					
Val	Val	Asn	Gly	Tyr	Ala	Ser	Ile	Leu	Leu	Leu	Thr	Ala	Ile	Ser	Ile
65					70				75					80	
Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	Leu	Arg	Tyr	Arg	Arg	Ile	Arg
85						90						95			
Thr	Pro	Arg	Arg	Ala	Lys	Val	Leu	Ile	Leu	Leu	Val	Trp	Val	Leu	Ala
100					105					110					
Leu	Leu	Leu	Ser	Leu	Pro	Pro	Leu	Leu	Phe	Ser	Trp	Leu	Arg	Thr	Val
115					120					125					
Glu	Glu	Gly	Asn	Thr	Thr	Val	Cys	Leu	Ile	Asp	Phe	Pro	Glu	Glu	Ser
130					135					140					
Val	Lys	Arg	Ser	Tyr	Val	Leu	Leu	Ser	Thr	Leu	Val	Gly	Phe	Leu	Leu
145					150				155				160		
Pro	Leu	Leu	Val	Ile	Leu	Val	Cys	Tyr	Thr	Arg	Ile	Leu	Arg	Thr	Leu
165					170						175				
Arg	Lys	Ser	Ala	Arg	Ser	Gln	Arg	Ser	Leu	Lys	Arg	Arg	Ser	Ser	Ser
180					185					190					
Glu	Arg	Lys	Ala	Ala	Lys	Met	Leu	Leu	Val	Val	Val	Val	Val	Phe	Val
195					200					205					
Leu	Cys	Trp	Leu	Pro	Tyr	His	Ile	Val	Leu	Leu	Asp	Ser	Leu	Cys	
210					215					220					
Leu	Leu	Ser	Ile	Trp	Arg	Val	Leu	Pro	Thr	Ala	Leu	Leu	Ile	Thr	Leu
225					230				235				240		
Trp	Leu	Ala	Tyr	Val	Asn	Ser	Cys	Leu	Asn	Pro	Ile	Ile	Tyr		
245					250										

<210> 75  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:pfam00001  
 7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 75  
 Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
 1 5 10 15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
 20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
 35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
 50 55 60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
 68

65	70	75	80
Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg			
85		90	95
Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala			
100		105	110
Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val			
115		120	125
Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser			
130		135	140
Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu			
145		150	155
Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu			
165		170	175
Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser			
180		185	190
Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val			
195		200	205
Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys			
210		215	220
Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu			
225		230	235
Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr			
245		250	
<210> 76			
<211> 254			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence:pfam00001			
7tm_1, 7 transmembrane receptor (rhodopsin family)			
<400> 76			
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg			
1	5	10	15
Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu			
20		25	30
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly			
35		40	45
Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe			
50		55	60
Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile			
65		70	75
Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg			
85		90	95
69			

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
 100 105 110  
 Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
 115 120 125  
 Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
 130 135 140  
 Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
 145 150 155 160  
 Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
 165 170 175  
 Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
 180 185 190  
 Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val  
 195 200 205  
 Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
 210 215 220  
 Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
 225 230 235 240  
 Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
 245 250  
  
 <210> 77  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:pfam00001  
 7tm\_1, 7 transmembrane receptor (rhodopsin family)  
  
 <400> 77  
 Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
 1 5 10 15  
 Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
 20 25 30  
 Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
 35 40 45  
 Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
 50 55 60  
 Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
 65 70 75 80  
 Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
 85 90 95  
 Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
 100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
145 150 155 160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
165 170 175

Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val  
195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
245 250

<210> 78

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00001  
7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 78

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
1 5 10 15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
50 55 60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
65 70 75 80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
85 90 95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser

130	135	140
Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu		
145	150	155
Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu		
165	170	175
Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser		
180	185	190
Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val		
195	200	205
Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys		
210	215	220
Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu		
225	230	235
Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr		
245	250	
 <210> 79		
<211> 254		
<212> PRT		
<213> Artificial Sequence		
 <220>		
<223> Description of Artificial Sequence:pfam00001		
7tm_1, 7 transmembrane receptor (rhodopsin family)		
 <400> 79		
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg		
1	5	10
15		
Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu		
20	25	30
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly		
35	40	45
Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe		
50	55	60
Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile		
65	70	75
80		
Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg		
85	90	95
Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala		
100	105	110
Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val		
115	120	125
Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser		
130	135	140
Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu		
145	150	155
160		

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
165 170 175

Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val  
195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Asp Ser Leu Cys  
210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
245 250

<210> 80

<211> 981

<212> DNA

<213> Homo sapiens

<400> 80

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gtatccagg actgcaatct tcacatcttt ggctggctat ctcactgagt gccatgtaca 120  
tcatagccct gtttagaaac accctcatacg tgactgcaat ctggatggat tccactcgcc 180  
atgagcccat gtattgcttt ctgtgtgttc tggctgtgt ggacattgtt atggcctcct 240  
ccgtggtacc caagatggtg agcatcttc gtcgggaga cagctccatc agcttttagtg 300  
cttgtttac tcagatgttt tttgtccact tagccacagc tggagacg gggctgctgc 360  
tgaccatggc ttttgaccgc tatgtagcca tctgcaagcc tctacactac aagagaattc 420  
tcacgcctca agtgatgctg ggaatgagta tggccgtcac catcagact gtcacattca 480  
tgactccact gagttggatg atgaatcatc taccttctg tggctccaat gtgggtgtcc 540  
actcctactg taagcacata gctttggcca ggtagcatg tgctgacccc gtggccagca 600  
gtctctacag tctgattggc tcctctctta tggtgggctc tggatgtggcc ttcattgctg 660  
cctcctataat cttaaattctc agggcagttat ttgatctctc ctcaaagact gtcagttga 720  
aagcattaaag cacatgtggc tcccatgtgg gggatgtggc tttgtactat ctacctggga 780  
tggcatccat ctatgcggcc tgggtggggc aggatatagt gcccctgcac acccaagtgc 840  
tgctagctga cctgtacgtg atcatcccaag ccactttaaa tcccatcatc tatggcatga 900  
ggaccaaaca attgctggag ggaatatgga gttatctgat gcactgtcct cttgaccac 960  
tccaacctgg gttcatgaac a 981

<210> 81

<211> 317

<212> PRT

<213> Homo sapiens

<400> 81

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
1 5 10 15

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
20 25 30

Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Leu  
35 40 45

Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
50 55 60

Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140  
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met  
 145 150 155 160  
 Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn  
 165 170 175  
 Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala  
 180 185 190  
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
 195 200 205  
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
 210 215 220  
 Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys  
 225 230 235 240  
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
 245 250 255  
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile  
 260 265 270  
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
 275 280 285  
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
 290 295 300  
 Leu Glu Gly Ile Trp Ser Tyr Leu Met His Cys Pro Leu  
 305 310 315

<210> 82  
 <211> 982  
 <212> DNA  
 <213> Homo sapiens

<400> 82  
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 ggtatcccg gactgaatc ttcacatctt tggctggcta tctcaactgag tgccatgtac 120  
 atcatagccc tggtagggaaa caccctcatac gtgactgcaa tctggatggaa ttccactcg 180  
 catgagccca tgtattgctt tctgtgtgtt ctggctgctg tggacattgt tatggcctcc 240  
 tcgggtgtac ccaagatgggt gaggcatcttc tgctcggag acagctccat cagcttttagt 300  
 gcttgtttca ctcagatgtt ttttgtccac ttagccacag ctgtggagac ggggctgctg 360  
 ctgaccatgg cttttgaccg ctatgtagcc atctgcaagc ctctacacta caagagaattt 420  
 ctcacgccttc aagtgtatgtt gggaaatgagt atggccgtca ccatcagagc tgcacatcc 480

atgactccac tgagttggat gatgaatcat ctaccttct gtggctccaa tgtggttgtc 540  
cactcctact gtaagcacat agcttggcc aggttagcat gtgctgaccc cgtgcccagc 600  
agcctctaca gtctgattgg ttccctctt atggggct ctgatgtggc cttcattgct 660  
gcctcctata tcttaattct cagggcagta tttgatctct cctcaaagac tgctcagttg 720  
aaagcattaa gcacatgtgg ctcccatgtg ggggttatgg ctttgtacta tctacctggg 780  
atggcatcca tctatgcggc ctgggtgggg caggatata gtcacccatgca caccbaagtg 840  
ctgctagctg acctgtacgt gatcatccca gcccacttaa atcccatcat ctatggcatg 900  
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<210> 83  
<211> 324  
<212> PRT  
<213> Homo sapiens

<400> 83  
Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
1 5 10 15  
Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
20 25 30  
Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Leu  
35 40 45  
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
50 55 60  
Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
65 70 75 80  
Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
85 90 95  
Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
100 105 110  
Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
115 120 125  
Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
130 135 140  
Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met  
145 150 155 160  
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn  
165 170 175  
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala  
180 185 190  
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
195 200 205  
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
210 215 220  
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys  
225 230 235 240  
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
75

245

250

255

Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile  
260 265 270

Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
275 280 285

Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
290 295 300

Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His Ser  
305 310 315 320

Asn Leu Gly Ser